

# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_

Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

12-366  
7E09

**Search Topic:**

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

**STAFF USE ONLY**

Date completed: 12-10-98

Searcher: Bob X8-4291

Terminal time: 5

Elapsed time: prep 10

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: 6

**Search Site**

STIC

CM-1

Pre-S

**Type of Search**

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

**Vendors**

IG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

MP3 Other



(ALL)

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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protein - protein database search, using Smith-Waterman algorithm	srch_pp	wed dec 9 19:15:56 1998:	MasPar time 27.66 Seconds
			547.553 Million cell updates/sec

title: >US-08-455-970-12  
    scription: (1-936) from US08455970.pep  
    fect Score: 6217

scoring table:

searched: 131922 seqs, 16180660 residues

post-processing: Minimum Match 0% Listing first 45 summaries

```
a:genesis32 1:part1 2:part2 3:part3 4:part4 5:parts 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29
```

Mean 37.888; variance 222.402; scale 0.170

Bre. No. is the number or results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	6217	100.0	977	19	W03942 LkT GnRH protein fusi	0.00e+00
2	6193	99.6	936	7	R34547 GnH-leukotoxin gene	0.00e+00
3	6135	98.7	1069	9	R52748 Bovine IFNgamma/LkT C	0.00e+00
4	6135	98.7	1069	21	W13867 Chimeric Protein #2.	0.00e+00
5	6128	98.6	926	3	R14482 LkT352	0.00e+00
6	6128	98.6	926	7	R34545 Leukotoxin 352 produc	0.00e+00
7	6128	98.6	926	10	R50291 Recombinant leukotoxi	0.00e+00
8	6117	98.4	924	8	R42378 Recombinant leukotoxi	0.00e+00
9	6117	98.4	924	8	R42380 Recombinant leukotoxi	0.00e+00
10	6117	98.4	924	8	R42385 Recombinant leukotoxi	0.00e+00
11	6119	98.4	926	19	W03945 P. haemolytica trunca	0.00e+00
12	6100	98.2	943	7	R34546 Somatostatin-leukotox	0.00e+00
13	6100	98.1	951	7	R34548 Rotavirus VP4-leukoto	0.00e+00
14	6094	98.0	924	3	R10889 Leukotoxin 352 encode	0.00e+00
15	6057	97.4	1098	21	W13866 Chimeric Protein #1	0.00e+00
16	6050	97.4	1098	4	R22103 Bovine II-2 - LkT fusi	0.00e+00
17	6047	97.3	1098	9	R52747 Bovine II-2/LkT chime	0.00e+00
18	6016	97.2	1052	10	R42386 Leukotoxin 352 produc	0.00e+00

				0.00e+00
19	6037	97.1	R07167	105kD PTX protein of
20	6037	97.1	R60072	PtxA protein of Paste
21	6022	96.9	R15159	Leukotoxin from P. ha
22	9425	79.2	W07637	P. suis leukotoxin ge
23	4254	68.4	W22156	ApxIC protein.
	4254	68.4	R12561	APPa haemolysin antag
	25	68.3	1049	APXIIIB protein.
	25	68.3	W22159	Leukotoxin ApptIIIA.
	26	41.3	1244	APXIA protein.
	27	36.9	1022	LhaA (low homology to
	28	2244	1023	LKT-GIRK protein fusi
	29	2223	15	1.97e-150
	35.8	544	19	1.97e-148
	30	1334	10	1.39e-144
	30	2167	1334	IktA::lacz fusion pro
	31	2160	3	IktA::lacz fusion prod
	32	2056	1403	IktA::lacz fusion pro
	33	1785	17	2.92e-136
	34	893	1522	Enterohaemorrhagic E.
	35	896	14.4	Sequence of the catal.
	36	893	14.4	3.51e-52
	37	885	14.4	Sequence of part of a
	38	453	1445	Adenyl cyclase from B
	39	448	7.3	N-terminal deleted ad
	40	440	7.2	B. pertussis adenylyc
	41	443	7.1	B. bronchiseptica ade
	42	281	4.5	B. bronchiseptica ade
	43	276	4.4	B. pertussis adenylyc
	44	223	3.6	Actinobacillus antige
	45	215	3.5	Sequen of a-Part
				Mannuronan C-5-peptimer
				Pseudomonas fluoresce
				2.44e-05

ALIGNMENTS

RESULT	
1	W03942 standard; Protein: 977 AA.
ID	W03942;
AC	W03942;
DT	20-NOV-1996 (first entry)
DE	LKT-GnRH protein fusion from pcB113.
KW	Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH; fusion protein; immunogen; vaccine; fertility control; contraceptive; sterilisation.
KW	Chimeric Pasteurella haemolytica A1 strain B122;
OS	Chimeric synthetic.
Key	Location/Qualifiers
FH	.
FT domain	1..929 /label= LKT
FT	927..977 /label= GnRH_repeat_domain
FT	W0624675-A1.
PN	

PU 13-AUG-1996; CA049.  
 PF 24-JAN-1996; CA049.  
 PR 10-FEB-1995; US-387156.  
 PA (USA) UNIV SASKATCHEWAN.  
 PI Mauns JG, Potter AA;  
 WPI: 95-384447/38.  
 DR N-PSDB; T37176.  
 PT Gonadotropin releasing hormone multimer fusion proteins - with  
 leukotoxin polypeptide for increased immunogenicity, useful in  
 antifertility vaccine prodn.  
 PS Claim 7: Fig 5A-5H: 87DP; English.  
 CC A chimeric protein (WO3842) is composed of a fusion between  
 CC a truncated leukotoxin (LKT-352) from Pasteurella haemolytica (see  
 CC also WO3845) and a 4-copy gonadoliberin-releasing hormone (GnRH)  
 CC repeat sequence (see also WO3944). It is the product of a  
 CC chimeric gene (T37176) produced by ligating a synthetic sequence  
 CC for the 4-copy GnRH into vector pAA352 (ATCC 68283), which carries  
 CC the LKT-352 gene. Recombinant plasmid pCB113 (LKT 352.4 copy  
 CC GnRH; ATCC 69749) was obtd. Escherichia coli transformants  
 CC produced the chimeric protein, which is useful as a vaccine for  
 CC fertility control, esp. immunological sterilisation of  
 CC domestic or farm animals.  
 Sequence 977 AA;  
 SQ

Matches	936; Conservative	0; Mismatches	0;	Indels	0;	Gaps	0;
b	1 malvidlspktgakkillyipqnyqydeqqgqlglvkaaeelgivqreenmtia	60					
b	1 MATVIDLSPKTGAKKILLYIPQNYQYDEQQGQLGLVKAEEELGIVQREENMTIA	60					
y	61 qtsigtqtaigtergivlsapdklqkqalgaaesivqnankaktvlgisq	120					
b	61 QTSIGTQTAIGTERGIVLSAPDKLQKQALGAESIVQNANKAKTVLGISQ	120					
y	121 ilgsvalgmdidealqnsnqhalaakagilettslienansyktldfgeqisqfgskl	180					
b	121 ILGSVALGMDIDEALQNSNQHALAAGILETTSlienansyktldfgeqisqfgskl	180					
y	121 IIGSVLADMIDDEALQNSNQHALAAGILETTSlienansyktldfgeqisqfgskl	180					
b	181 qniqglgtlgdiklnnigldkaglgldvtsgatavaladknastakvgagfela	240					
b	181 QNIQGLGTLDIKLNNGDIDKAGLGLDVTSGATVALADKNASTAKVGAGFELA	240					
y	241 nqvvgnitkavssyiladrvagsisstpdvaliastvsliaplafagiadkfhnksl	300					
b	241 NQVGNITKAVSSYILADRVAGSIGSTPDVALIASTVSЛИАПЛАФАГИАДКФНХСЛ	300					
y	301 esaerffkklygdydnlaeyqrqtgtidastvtaintalaaggvsaagsyiasia	360					
b	301 ESAERFFKKLYGDYDNLAEYQRQTGTIDASTVTAINTALAAGGVSAAGSYIASIA	360					
y	361 llysgitgrist1lqskmgfehankthnkivewknhnghnyfengdyarlanlqd	420					
b	361 LLYSGITGRIST1LQSKMGFEHANKTHNKIVEWKNHNGHNYFENGDYARLANLQD	420					
y	421 nmkflnlmklnkelqervariaitqggwdnnqldlagisrigekvlsgkayvdafeegkhika	480					
b	421 NMKFLLNLMKLNKELEQSERVIAITQGGWDNNQLDLAGISRIGEKVLSGKAYDAFEKGHKHA	480					
y	481 dk1qgdsang1idvsnspkakcahlfptpltgtehrerqtkkeyitklininvd	540					
b	481 DK1QGDSANG1IDVSNSPKAKCAHLFPTPLTGTEHRERQTKKEYITKLININVD	540					
b	541 swkitdgassstfdltvnvqrqgfehdngvktkektiaklggeddnvfvsgttei	600					
b	541 SWKITDGASSSTFDLTVNVRQGFEHDNGVKTKEKTIAKLGGEDDNVFVSGSTEI	600					
b	601 dggegydrhyrsrgnygaltidatketedgysytvrnfvetgkahlhevsthtalvgree	660					
b	601 DGGEGYDRHYRSRGNYGALTIDATKETEDGYSYTVRFVETGKALHEVSTHTALVGREE	660					
y	661 kierhrsnqhaayyytdtlkaree1gtsndifgsksfndsfngfdgvtidagn	720					
b	661 KIERHRSNQHAAYYYTDTLKAREE1GTSNDIFGSKSFNDSFNGFDGVTIDAGN	720					
b	721 dr15ggkgdd1qgqddfdgkqndllhggkgddifvhkrgndd1itsqndks	780					
b	721 DR15GGKGDD1QGQDDFDGKQNDLLHGGKGDDIFVHKRGNDD1ITSQNDKS	780					
b	781 fdsdnklkd1tfekvkhnlvtnskkekvtqnywreadfakvepnykatdkdekieqq	840					
b	781 FDSDNKLKD1TFEKVKhNLVTNSKEKVNTQNYWREADFAKEPVNYKATDKDEKIEIQQ	840					
y	841 ngeritskydd1akqngktqdelkskvrdnyellksknvntsldklissysaftssn	900					
b	841 NGERITSKYDD1AKQNGKTQDELKSKVRDNYELLKSKNVNTSLDKLISSYSAFSSN	900					
y	901 dsrnvlaptsmldqs1ss1qfargsqhwsg1rpq	936					
b	901 DSRNVLAPTSMLDQS1SS1QFARGSQHWSG1RPQ	936					
y	301 esyerffkklygdydn1laeyqrqtgtidastvtaintalaaggvsaagsviaspia	360					
b	301 ESYERFFKKLYGDYDN1LAEYQRQTGTIDASTVTAINTALAAGGVSAAGSYIASPIA	360					
b	361 llvsgitgry1st1qyskcamfehvanklhkn1vewlkhngkbyfengdylan1qd	420					
b	361 LLVSGITGRY1ST1QYSKCAMFEHVANKLHKN1VEWLKHNGKBYFENGDYLAN1QD	420					
b	421 nmkflnlmklnkelqervai1tqgqwdnnqldagisrigekvyskayvdafesgkhika	480					
b	421 NMKFLLNLMKLNKELEQSERVAI1TQGGWDNNQLDAGISRIGEKVSKAYVDAFEKGHKHA	480					
vector:	LKT	352;	flanking:	recombinant:	antigen:	somatostatin:	
vector:	LNK	352;	gene fusion prod.				

QY 481 DKLVQLDSANGTIDVNSGKARTQHILFRTPJPGTEHREVQTCRYEYTAKLNENRVD 540  
 Db 541 swkitdgaasstfdltnvqrqfieldagnrtktktkialkgeddnvfvgsgtei 600  
 QY 541 SWKITDGAASSFDLTVNRIGFIELDGNANTKTKEKTKIAKLGESDDNVEVGSGTEI 600  
 Db 601 dggeydrhysrgnygaltidatketeqgsytvnrfvetskalhevtsttalyvngree 660  
 QY 601 DGEGYDRHYSRGNYGALTATKETEQGSYTVNRFVETSALKALHEVTSTHALVNREE 660  
 Db 661 kieyrhsnnqhhagyyktktlkaveeigtshtndifgskfrdafrggdrydtidgdn 720  
 QY 661 KIEYRHSSNOHHAGYYKTDTLKAVEEIGTSHTNDIFGSKFRDAFNGDGTIDNDGN 720  
 Db 721 dr1fgkqddidggnoddfidgkgnndlhgkgddifvhrgndnditdsndkls 780  
 QY 721 DR1FGGKQDDIDGGNODDFIDGGKGNDLIHGKGDDIFVHKGDNIDTSDGNDKLS 780  
 Db 781 fdsnlkaltfekvhnlvntskkekvtqnfreadfakevpnykatdekieeiggg 840  
 QY 781 FDSNLKALTFEKVHNLTITVKKEKVTQWFREADFAKEVPNKATDKKEIEIGO 840  
 Db 841 ngeritskqvddiakqngktqdelskvdvnyellkhksknvntsldklissysafssn 900  
 QY 841 NGERITSKQVDDIAKNGKTIQDELSKVDVNYELLKHSKNVNTSLDKLISSSVAFSSN 900  
 Db 901 dsrnvlrvaptmldqsllsqfargshwsglyrpq 936  
 QY 901 DSRNVLVAPTMULDQSLLSQFARGSHWSGYLRPQ 936

RESULT 3  
 ID R52748 standard; Protein: 1069 AA.  
 AC R52748;  
 DT 01-JUL-1994 (first entry)  
 DE Bovine IFNgamma/Ltk chimeric protein encoded by plasmid PAA497.

KW Bovine; interleukin-2; IL2; P. haemolytica; leukotoxin; Ltk; IFN;  
 KW chromosome walking; fusion protein; vaccine; interferon; gamma;  
 KW monoclonal; polyclonal; antibody.  
 OS Pasteurella haemolytica - chimera  
 OS Bos taurus - chimera  
 FH Location/Qualifiers  
 FT 1..926  
 /note= "Recombinant leukotoxin peptide [split]"  
 FT peptide 927..1069  
 /note= "Bovine IFNgamma"

PN US5273888-A.

PD 28-DEC-1993.

PF 22-AUG-1990; 571301.

PR 16-OCT-1991; US-77715.

PA (CIBA) CIBA GEIGY CANADA LTD.

(U.S.A.) UNIV SASKATCHEWAN.

PI Campos M., Hughes HPA, Potter A;

DR WPI: 94-00668/01.

N-PDB: 054213

PR Immunogenic fusion proteins of gamma-interferon and immunogenic

PR leukotoxin - used in vaccines and to raise monoclonal and polyclonal

PR antibodies.

Disclosure: Pig 7; 56pp; English.

This sequence represents a fusion between bovine leukotoxin (Ltk). The  
 CC (IFNgamma) and Pasteurella haemolytica leukotoxin (Ltk) gene, itka, was isolated from a gene library of P.  
 CC haemolytica by chromosome walking. Immunogenic fusion proteins  
 CC such as this can be used in vaccine compositions. It can also be  
 CC used to raise mono- and polyclonal antibodies.  
 Sequence 1069 AA;

QY	481 DKLVQLDSANGTIDVNSGKARTQHILFRTPJPGTEHREVQTCRYEYTAKLNENRVD 540	Db	matvidslfpktgalkiiiyipqnyqydgfegngiqdlykaeelgivqeernniata 60
Db	541 swkitdgaasstfdltnvqrqfieldagnrtktktkialkgeddnvfvgsgtei 600	QY	1 MATVILSPATGAKKILLYPQNQYDTFOQNGQDLVKAEEELGIVQEERNNIATA 60
QY	541 SWKITDGAASSFDLTVNRIGFIELDGNANTKTKEKTKIAKLGESDDNVEVGSGTEI 600	Db	61 qtslgtiqtaiglttergvilsapqidklqlktqaggalsaesivqnankaktvlgsgis 120
Db	601 dggeydrhysrgnygaltidatketeqgsytvnrfvetskalhevtsttalyvngree 660	QY	61 QTSLGQTQAIGLTERGVILSAPQDQLKLORKASQALGSAESTIQNANFKTVLGSQIS 120
QY	601 DGEGYDRHYSRGNYGALTATKETEQGSYTVNRFVETSALKALHEVTSTHALVNREE 660	Db	121 lgsvlagtdideamnnshahalakagoltnstieniansrktdfeqisqfski 180
Db	661 kieyrhsnnqhhagyyktktlkaveeigtshtndifgskfrdafrggdrydtidgdn 720	QY	121 TLGSVLAGMDLEALNNNSQNHALAKAGELNTSUTENTANSVKTDEFQDQFSKL 180
QY	661 KIEYRHSSNOHHAGYYKTDTLKAVEEIGTSHTNDIFGSKFRDAFNGDGTIDNDGN 720	Db	181 qnkgqlgtgdklnnigldkagigldividsglisgetaialdnastakkvgagfela 240
Db	721 dr1fgkqddidggnoddfidgkgnndlhgkgddifvhrgndnditdsndkls 780	QY	181 QNKGQLGTGDKLNKGKLGKAGLGLDVISLLSCATALVLDKNASTAKVKGRGFELA 240
QY	721 DR1FGGKQDDIDGGNODDFIDGGKGNDLIHGKGDDIFVHKGDNIDTSDGNDKLS 780	Db	241 nqvgvnitkavssyllaqryaagllssttpvaaliastvsaisplafagiadkfhnaks1 300
Db	781 fdsnlkaltfekvhnlvntskkekvtqnfreadfakevpnykatdekieeiggg 840	QY	241 NOVGGNTKAVSSYTLAQRYAAGLSSGTGAALIYSTVSALISPLAFAGIADKFHNAKSL 300
QY	781 FDSNLKALTFEKVHNLTITVKKEKVTQWFREADFAKEVPNKATDKKEIEIGO 840	Db	301 esyaerfkleydgdnlalaeyqrgtctidaesvtantalaiaqgrsaagsvtaspia 360
Db	841 ngeritskqvddiakqngktqdelskvdvnyellkhksknvntsldklissysafssn 900	QY	301 ESYAERFKQGYDGDNLALAEYORGFTGTDASVTAINTALLAIAQGVSAAAGSVTASPIA 360
QY	841 NGERITSKQVDDIAKNGKTIQDELSKVDVNYELLKHSKNVNTSLDKLISSSVAFSSN 900	Db	361 llvsgitgvistlqycskqanfehavkhnkivekenhkgknyfengdarylanqd 420
Db	901 dsrnvlrvaptmldqsllsqfargshwsglyrpq 936	QY	361 LLVSGITGVISTLQYSKQANFERVANKKIVEKENHKGKNFENGTDARLNQD 420
QY	901 DSRNVLVAPTMULDQSLLSQFARGSQHWSGYLRPQ 936	Db	421 nmkflnlneklaqerviaitaqqgwonnigdlagisrlgekvlsgkayydafeegkhika 480
Db	481 dkivqldsaangidvnsrnsgrktqhlfcp1ptgtctehvqgkkeyitklnhrrvd 540	QY	421 NMKFLNLNEKEQAAERVIAITQQDQDNNGDLAGISRLGEKVLSGRAYDAFEGRHKIA 480
Db	541 swkitdgaasstfdltnvqrqieldagnrtktktiaklgdgvfvgsgttei 600	Db	481 DKLYQLDSDANGTIDVNSGKARTQHILFRTPJPLPTCTEHRSVQKYEYTKLNINRVD 540
QY	541 SWKITDGAASSFDLTVNRIGFIELDGNANTKTKEKTKIAKLGEGDNDVFGSGTTEI 600	Db	541 SWKITDGAASSTFDLTVNRIGFIELDGNAGVTRKETKIAKLGEGDNDVFGSGTTEI 600
Db	601 dggegydrhysrgnygaltidateteqsytrnfvetgkahlhevtshtalvgnre 660	QY	541 SWKITDGAASSTFDLTVNRIGFIELDGNAGVTRKETKIAKLGEGDNDVFGSGTTEI 600
QY	601 DGEGYDRVHRSRGNYGAALTDATETEQSYTRNFWFETGKALHEVTSHTALVGNRE 660	Db	601 dggegydrhysrgnygaltidateteqsytrnfvetgkahlhevtshtalvgnre 660
Db	661 kieyrhsnnqhhagyyktktlkaveeigtsndifgkfsndafqgdrtdlgdgn 720	QY	601 DGEGYDRVHRSRGNYGAALTDATETEQSYTRNFWFETGKALHEVTSHTALVGNRE 660
Db	721 dr1fggkqddidggnoddfidgkgnndlhgkgdodfhrgkgdnditdsndkls 780	QY	661 KIEYRHSSNOHHAGYZKDTLKAVEELIGTSHNDIFKGSKENDAFNGGYDVTIDCGNDGN 720
QY	721 DR1FGGKQDDIDGGNDDDFDGKNDLILLGGKDDITHRKGONDITDSGNDKLS 780	Db	721 DR1FGGKQDDIDGKNDLILLGGKDDITHRKGONDITDSGNDKLS 780
Db	781 fsdsnlkaltfekvhnlvntskkekvtqnfreadakevpnykatdekieeiggg 940	QY	721 DR1FGGKQDDIDGGNDDDFDGKNDLILLGGKDDITHRKGONDITDSGNDKLS 780
QY	781 FSDSNLKALTFEKVHNLTITVKKEKVTDEFQDQFSKL 940	Db	781 FSDSNLKALTFEKVHNLTITVKKEKVTDEFQDQFSKL 940
Db	841 ngeritskqvddiakqngktqdelskvdvnyellkhksknvntsldklissysafssn 900	QY	781 FSDSNLKALTFEKVHNLTITVKKEKVTDEFQDQFSKL 940
QY	841 NGERITSKQVDDIAKNGKTIQDELSKVDVNYELLKHSKNVNTSLDKLISSSVAFSSN 900	Db	841 ngeritskqvddiakqngktqdelskvdvnyellkhksknvntsldklissysafssn 900
AC	WJ3867 standard; Protein: 1069 AA.	AC	WJ3867;
DT	12-MAY-1997 (first entry)	DT	12-MAY-1997
DE	Chimeric Protein #2.	DE	Chimeric Protein #2.
KW	RTX cytotoxin; cytokine; immunogen; chimeric protein; vaccine;	KW	RTX cytotoxin; cytokine; immunogen; chimeric protein; vaccine;
KW	IFN; leukotoxin; gamma IFN; leukotoxin; gamma IFN; leukotoxin;	KW	IFN; leukotoxin; gamma IFN; leukotoxin; gamma IFN; leukotoxin;
KW	Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;	KW	Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;

RESULT 4  
 ID WJ3867 standard; Protein: 1069 AA.

AC WJ3867;

DT 12-MAY-1997

(first entry)

DE Chimeric Protein #2.

KW RTX cytotoxin; cytokine; immunogen; chimeric protein; vaccine;

KW IFN; leukotoxin; gamma IFN; leukotoxin; gamma IFN; leukotoxin;

Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;

Query Match 98.7%; Score 6135; DB 9; Length 1069;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 1069 AA;

KW fibrinous pneumonia; cattle; therapy.	Qy 541 SWKITDGAASSTFDLTVNYQRIGIELDNAGNTTKTETKIIAKLGEIDDNVFGSGTTIEI 600
OS SYnthetic.	Db 601 dggegydrhysqnygaltidaeketegsgtynrfvtgkhalhevsthalvgmre 660
PN PD 14-JAN-1997; A. 571301.	Db 601 DGGCYDRHYSRNYGATIDATKETEGSGTYNRFVTGKALHEVSTHALVGNEE 660
PR 22-AUG-1990; US-571301.	Qy 601 KIEFRHSNNQHHAGYYTktlkavvee19tshdifikgsfndafngdgvtldgnagn 720
PR 16-OCT-1991; US-77715.	Db 661 kieyrhsnnqhhagyytktlkavvee19tshdifikgsfndafngdgvtldgnagn 720
PR 20-DEC-1993; US-170126.	Qy 661 KIEFRHSNNQHHAGYYTktlkavvee19tshdifikgsfndafngdgvtldgnagn 720
PA (CIBA) CIBA GEIGY CANADA LTD.	Db 721 drlfgkgddldggdgdffdgkgnldlhggkdddfvhrkgdgnndtsdgnkls 780
PA (U.S.A.) UNIV SASKATCHEWAN.	Qy 721 DRLFGKGDDLDGGDGDFFDGKGNLDLHGKGDDDFVRKGDNIDITSDGNDKLS 780
Campos M. Hughes HPA. Potter A;	PT Immunoenic chimeric proteins comprising cytokine linked to RTX toxin useful in vaccines, esp. against shipping fever in cattle
DR WPI: 97-09529/09.	PS Claim 13; Column 37-46; 56pp; English. W13866 and W13867 represent immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine gamma interferon (gamma IFN) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from interleukin-2 (IL-2) and gamma IFN, linked to at least one RTX toxin epitope (preferably the sequence shown in W13865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially LKT32. The chimeric proteins can be used for the production of vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by <i>P. haemolytica</i> , including shipping fever in cattle.
N-PSDB; T60033.	SQ Sequence 1069 AA;
PT	RESULT 5
PS	ID R14482 standard; Protein: 926 AA.
CC	AC R14482;
CC	DT 15-JAN-1992 (first entry)
CC	DE LKT352.
CC	KW Antigen; leukotoxin; vaccine; lktA.
CC	OS WO9115237-A.
CC	PD 17-OCT-1991.
CC	PF 17-OCT-1991; CA0170.
CC	PR 05-APR-1990; US-504850.
CC	PA (U.S.A.) UNIV SASKATCHEWAN.
CC	PI Acres SD, Baruk Lk, Potter AA, Lawman MJP;
CC	DR WPI: 91-24967/44.
CC	PT Vaccines for Pasteurella haemolytica infection in cattle - composite sub-unit antigens from <i>P. haemolytica</i> fimbrial protein, plasmid receptor, 50 K outer membrane protein and leukotoxin.
CC	PT Disclosure: Fig 5; 92pp; English.
CC	LKT352 is 98% homologous with authentic leukotoxin and migrates to the same position on gels.
CC	The LKT352 gene was pred. as follows: lktA, an MaeI fragment, the 5' AhAII fragment from lktA while the other, pAA345, contained the entire MaeI fragment. Clone PAA342 expressed a truncated full length leukotoxin at high levels while pAA345 expressed full length leukotoxin at very low levels. The 3' end of the lktA gene of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to yield pAA352 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other <i>P. haemolytica</i> antigens, e.g. fimbrial protein, plasmid receptor or 50K outer membrane protein. The vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp. shipping fever pneumonia.
CC	See also R14481, 83, 84 and 85.
CC	SQ Sequence 926 AA;
Db 61 qtslgqtgaatgttergivisaqpidkkllgktaqalgaaesi9qnankaktvlgis 120	Query Match Best Local Similarity 100.0%; Score 6135; DB 21; Length 1069;
Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Db 1 matvidlspfkpgakkilypqnyqydtteggnglqdlyvkaaeelgivgreenriata 60	Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATVIDLSPFKPGAKKILYLPQNYQYDTEGGNGLQDLVKAEEELGIVGREENRIATA 60	Db 1 matvidlspktgakkilypqnyqydtteggnglqdlyvkaaeelgivgreenriata 60
Db 61 qtslgqtgaatgttergivisaqpidkkllgktaqalgaaesi9qnankaktvlgis 120	Qy 1 MATVIDLSPFKPGAKKILYLPQNYQYDTEGGNGLQDLVKAEEELGIVGREENRIATA 60
Qy 61 QTSLGQTGATGTLTERGIVLSPAQIDKLQLQTKAGAOGLSAEITVQNANKAKTVLGSQS 120	Db 121 lgsvlqmddealqnnshalakagleltinsitensiansvk1defeqisofgsk1 180
Db 121 lgsvlqmddealqnnshalakagleltinsitensiansvk1defeqisofgsk1 180	Qy 121 IIGSVLAGMDDEALONNSHOHALAKAGLELTINSITENSANSVTLDEREQISFGSKL 180
Qy 121 IIGSVLAGMDDEALONNSHOHALAKAGLELTINSITENSANSVTLDEREQISFGSKL 180	Db 181 qnikiqigtgdklnnigldkqaglgldvisqtlsgataalvladknasrakkygagfela 240
Db 181 qnikiqigtgdklnnigldkqaglgldvisqtlsgataalvladknasrakkygagfela 240	Qy 181 QNIGKGLTGDKLNIGLDLGRGDLVISLGSATAALVLADKNASTAKKVGRGFELA 240
Qy 181 QNIGKGLTGDKLNIGLDLGRGDLVISLGSATAALVLADKNASTAKKVGRGFELA 240	Db 241 nqvvgnitkavssylaqraqaqlsstspralaistsvlaispafagiaidkfnhaks1 300
Db 241 nqvvgnitkavssylaqraqaqlsstspralaistsvlaispafagiaidkfnhaks1 300	Qy 241 NQVGNITKAVSSYLAQRAQLSSTSPPALAISTSVLAISPAGTADKENHAKSL 300
Qy 241 NQVGNITKAVSSYLAQRAQLSSTSPPALAISTSVLAISPAGTADKENHAKSL 300	Db 301 esyaerfkklgydgdnlaeyqrgtgidavtialaiaggysaaaagsviaspia 360
Db 301 esyaerfkklgydgdnlaeyqrgtgidavtialaiaggysaaaagsviaspia 360	Qy 301 ESYAERFKKLGYDGDNLAEYQRGTGTIDASVTAINTALLAAGGVSAAAGVIASPIA 360
Qy 301 ESYAERFKKLGYDGDNLAEYQRGTGTIDASVTAINTALLAAGGVSAAAGVIASPIA 360	Db 361 llvsgitgvistulgskqanfehankhnkiveweknghknkyfengydarylanlqd 420
Db 361 llvsgitgvistulgskqanfehankhnkiveweknghknkyfengydarylanlqd 420	Qy 361 LLVSGITGVISTILOQSKQAMFEHANKHNKIVEWENKNHGKNTFENGTDARYLANLQD 420
Qy 361 LLVSGITGVISTILOQSKQAMFEHANKHNKIVEWENKNHGKNTFENGTDARYLANLQD 420	Db 421 nmkf1lnlnkelqaerviaitqgqwdnnigldlagsrlgkvs1sgkayrdafeekhika 480
Db 421 nmkf1lnlnkelqaerviaitqgqwdnnigldlagsrlgkvs1sgkayrdafeekhika 480	Qy 421 NMKF1LNKELQAERVIAITQGQWDNNIGLDAGSRLGKVS1SGKAYRDAFEEKHKA 480
Db 481 dkvlqldsanidvsnsgkhtqhliftp1lptgtehrvrtgkveyitklninrvd 540	Db 481 DKVLQLDSANIDVSNSGKHTQHLIFTP1LPTGTEHRVRTGKVEYITKLNINRVD 540
Qy 481 DKVLQLDSANIDVSNSGKHTQHLIFTP1LPTGTEHRVRTGKVEYITKLNINRVD 540	Qy 481 DKVLQLDSANIDVSNSGKHTQHLIFTP1LPTGTEHRVRTGKVEYITKLNINRVD 540
Db 541 swkitdgaasstfdltnvvarqielndagnvtktketkia1k1egddnnfvsgstte1 600	Db 541 MATVIDLSPKTGAKKILYLPQNYQYDTEGGNGLQDLVKAEEELGIVQREERNNTATA 60

Db 61 qtslgltqtaigltergivlsapqidkkllqktkaggalgsaaasiqvnankatkvlsqiqs 120  
 Qy 61 QSLGLTQTAIGLTERGIVLSAPQIDKKLLQKTAKGGALGSAAASIQLVNVANKATKVLSQIQS 120  
 PR 16-OCT-1991; US-779171.  
 PR 14-OCT-1992; US-960932.  
 PR (UWSA-) UNIV SASKATCHEWAN.  
 PA Hughes HPA, Potter AA, Redmond MJ;  
 PI Hughes HPA, Potter AA,  
 DR WPI: 93-157482/18.  
 DR NPSDB; Q41317.  
 PT Immunological carrier system with enhanced immunogenicity -  
 PT comprises chimeric protein comprising leuco-toxin peptide or  
 PT homologous protein fused to antigen esp. somatostatin or  
 PT gonadotropin releasing hormone  
 PS Disclosure: Fig 3: 95pp; English.  
 CC Gene libraries of *P. haemolytica* A1 (strain B122) were constructed  
 CC in lambda gt1 and pUC13. Resulting clones were used to transform E.  
 CC coli and individual colonies were pooled and screened for reaction  
 CC with serum from calf which had survived a *P. haemolytica* infection  
 CC and that had been boosted with a conc. culture supernatant of P.  
 CC haemolytica to increase anti-leukotoxin antibody levels. Positive  
 CC colonies were screened for their ability to produce leukotoxin by  
 CC incubating cell lysates with bovine neutrophils and measuring the  
 CC release of lactate dehydrogenase from the neutrophils. A 4 kb  
 CC plasmid was isolated. Progressively larger clones were isolated by  
 CC chromosome walking to isolate full length recombinants of ca. 8 kb,  
 CC in pAA14. The clone was subjected to restriction enzyme digestion  
 CC to yield two clones, one expressing truncated leukotoxin at  
 CC high levels and the other expressing the full length leukotoxin at  
 CC low levels. The 3' end of the lktA gene from the full length clone  
 CC was ligated to the truncated gene clone to yield plasmid pAA352. The  
 CC clone was used to produce chimeric proteins by gene fusion with an  
 CC antigen coding sequence, e.g. the coding sequence of somatostatin,  
 CC gonadotrophin releasing hormone or rotavirus viral protein 4, i.e.  
 CC leukotoxin works as a carrier protein to bring about a larger  
 CC immune response than the antigen alone. Immunisation with these  
 CC antigens can regulate growth rate, lactation and reproductive efficiency.  
 See also R34546-8.  
 SQ Sequence 926 AA;

Query Match 98.6%; Score 6128; DB 7; Length 926;  
 Best Local Similarity 100.0%; Pred. No. 0; 0e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 matvidlsfpktgakkiliypqnygydteggnglqdvlvkaaeelgievqreerriata 60  
 Qy 1 MATVIDLSFPKTGAKKILYLPQNYGYDTEGGNGLQDVLVKAEEELGIEVQEERRIATA 60  
 Db 1 qtslgltqtaigltergivlsapqidkkllqktkaggalgsaaasiqlvnvankatkvlsqiqs 120  
 Qy 1 QTSLGLTQTAIGLTERGIVLSAPQIDKKLLQKTAKGGALGSAAASIQLVNVANKATKVLSQIQS 120  
 Db 1 11gvslagmdidealqnnsnghalakagleitnsliensiansvtkldefgeqisqfks1 180  
 Qy 1 11GVSLAGMDIDEALQNNSNQHAGYTTKDTLKAVEETIGTSNDIFGSKFEDAFNGDGVPIDGDGN 720  
 Db 1 drfggqddildggnddfiaggknddlhgkgddifurhkgndditcsedgndks 780  
 Qy 1 DRFGGKDDIDGGNGCDDDFIIGCKGNDLHKGKDDIFVHKRGDNDLITPSDGNDKLS 780  
 Db 1 fsdsnlrltfevkhnlvituskekvtlqnfreadfakcavpnykatdkkdeieeigq 840  
 Qy 1 FSSNLRLTFEVKHNLVITUSKKEKVTIONFREDFAKCVPNYKATDKKDEIEIGQ 840  
 Db 1 geritskqvddiaikngngktodelskvdyellkhsknrvtsdklissvsafssn 900  
 Qy 1 GERITSKQVDLIAIKNGKTIODELSKVDNELLKHSKNVTNSLDKLISSVSAFSSN 900  
 Db 1 dsrnvlvaptmsmlqslsllfqargs 926  
 Qy 1 DSRNVLVAPTMSDLQSLSSLQFARGS 926  
 PR 6  
 ID R34545; Standard; Protein; 926 AA.  
 AC R34545;  
 DT 23-AUG-1993 (first entry)  
 DE Leukotoxin 352 produced from pAA352.  
 KW Vector; Lkt 352; flanking; recombinant; antigen; somatostatin;  
 KW gonadotropin releasing hormone; rotavirus viral protein 4;  
 KW carrier protein; lactation; reproduction.  
 KW Pasteurella haemolytica.  
 OS WO308290-A.  
 PD 29-APR-1993.  
 PN 29-OCT-1992; CA0449.  
 PF 15-OCT-1992.

Qy 481 DKLVQDSDANSIIDIYNSGRAKTOHILFRPLLTGTEIRERVQTKYXYITKLNNINRYD 540.  
Db 541 swkitgaaasstfdlnvvarqieldnagnvtkcketkiaik1gegdanfvysgttei 600  
Qy 541 SWKITGAAASSTFDLNVVORIGIEDLDNAGNTKETKIAKUJEGDDNRFVCSGTTIEI 600  
Db 601 dgegydrhysrgygalidatketegsytnrfvetgkahlhevttshthalvgnree 660  
Qy 601 DGEGYDRVYRSRGNGLPDTDATEKETEQQSYTNRFVEGTTHALVGNRRE 660  
Db 661 kieyrhsnnghagytktdklaveeigshndifkgskfndafnggqvtdldgndgn 720  
Qy 661 KIEYRHISNNQHAGYTCKDTIKAVBELLGTSNDIFKGSKFNDAFNGGQVTDIDGNDGN 720  
Db 721 drifgqkddildggngdffdggknddlhgqkddifvhrikadgndndkls 780  
Qy 721 DRIFGGKGDIDLGGNGDDFLGGKNDLHGGKDDIFHRKGDDNLDTSQGNDKLS 780  
Db 781 fdsnplkdlfekvhnlytnsksekvtlqnwfreadfakewpykatzkdekleeiigq 840  
Qy 781 FDSNPKDLFEKVHNLYTNSKEKVTQNWFREADFAKEWPYKATKDEKBEIGQ 840  
Db 841 ngeritskqvddliakgngkitqdelkskvvrdnyellkhsknntsldklissvsaftssn 900  
Qy 841 NGERITSKQVDDLIAKGNGKTIODELSKQVYDNELLKHSKNNTNSLDKLISVSAFTSSN 900  
Db 901 dsrnvlvaptsmldssllsqfargs 926  
Qy 901 DSRNVLVAPTSMLDOSLSSLLQFARGS 926

RESULT 7  
ID R50291; standard; Protein: 926 AA.  
AC R50291;  
DT 06-OCT-1994 (first entry)  
DE Recombinant leukotoxin from plasmid pAA352.  
KW Vaccine; outer membrane protein; OMP; Haemophilus somnus;  
KW iron-regulated protein; leukotoxin; Pasteurella haemolytica;  
KW LKT352.  
OS CA20997\_07\_A.  
PD 03-JAN-1994.  
PR 29-JUN-1992; 099707.  
PA (UYS ) UNIV SASKATCHEWAN.  
PI Harland RU,  
Potter AA;  
DR WPI: 94-032909/12.  
DR N-PSDB; Q44760.  
PT Haemophilus somnus outer membrane protein extract - enriched with iron-regulated proteins, opt. contg.  
PT leuco-toxin antigens, for use as vaccine  
PS Claim 5; Fig 5; 78pp; English.

CC A vaccine comprising an outer membrane protein (OMP) extract of Haemophilus somnus enriched with iron-regulated proteins is new.  
The vaccine pref. further comprises an immunogenic Pasteurella haemolytica leukotoxin polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin homologous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352.  
Two expression constructs were made. One, pAA342, contained the 5'-AataII fragment of the lktA gene, while the other, pAA345, contained the entire lktA gene. pAA342 expressed a truncated leukotoxin peptide at high levels, while pAA345 expressed a full length leukotoxin at very low levels. Therefore, the 3' and 5' ends of the lktA gene were ligated in pAA344. Yielding plasmid pAA352.  
CC LKT352 or new leukotoxin is 98% homologous to authentic leukotoxin.  
CC NB: the protein sequence in Fig 5 comprises 926 amino acids, however this protein is described in the text as having 931 amino acids.  
CC Sequence 926 AA;

	Best Local Similarity 100.0%	Pred. No. 0.00e+00;	No. Mismatches 0;	Indels 0;	Gaps 0;
	Matches 926; Conservative 0;				
Db	1 matvidlspktagkakiiiyipqnyqydeggnglqdkvkaeelgleygreenntia	60			
Qy	1 MATVIDLSPKTAGKAKIIIYIPQNYQYDEGGNGLQDKVKAELGLEYGREENNTIA	60			
Db	61 qtsigtqtaiq tergiwvlsapqidkllqkttagqalsgaesivqankakavtsgiqs	120			
Qy	61 QTSGTQTAIQTERGIVLSPQAQDQKUQTRAGOALSASETIVONANKAKIVLGSQIS	120			
Db	121 ligsvlagmiddealqnsnqhalaqagleltnslienansvtkldfgeqisqfqsk1	180			
Qy	121 ILGSVLAGMIDDEALQNSNQHALAQAGLELTNSLIENIANSVTKLDFGEQISQFSQL	180			
Db	181 qniqkglgtlgdkkniggdkaglgldgvtsqllsataalvialdknastakkvgagfela	240			
Qy	181 QNIKGGLGTUDKURKINGGDKAGLGLDTSIGLISGATAVLADKNASTAKVAGGFBLA	240			
Db	241 nqygnitkavssyilagrvaaqslstsppvaaiastvslaisplaffqiadfnhaks1	300			
Qy	241 NOYGNITKAVSSYILAQRAAGLSSSTPPVAALIYSTSLAISPLAFAGIADFNHAKSL	300			
Db	301 esyerfkklglygdnllaeyleyqrgtgtdiasvtaintalaataggvsaaagsviassla	360			
Qy	301 ESTAERFKLGYGDNLNLALEYQRTGTIDASVTAINTALAATAGGVAAAAGSVIASPIA	360			
Db	361 llvesgitgristllqskamfehankiveweknhgknyfengydarlylan1qd	420			
Qy	361 LLVSGITGISTLQLYSQAMFEHVANKIHNKLVWEVKNHGKNYFENGYDARYLAN1QD	420			
Db	421 nmkfllnlnkelaervviaitqqwdnnigdlaqisrigkevlsqkarydafeegkhika	480			
Qy	421 NMKFLLNLNKELQARVIAITQQWDNNNGDLAGISRUEKYLGSKAYDGFEGKHKA	480			
Db	481 dkvlgldang1davsnqkaktgh1frtp11tpgchervqtghye1tklnlnvd	540			
Qy	481 DKLVQLDANG1DVSNSQKAKTOHILFRTP11TPGCHERVQTYKETKLNINVD	540			
Db	541 swkitdgassstfoltnvqrigieldnagnaevktktk1aki1gegdnfnvfgsgttee	600			
Qy	541 SWKITDGASSSTFDLTVNQRIGLDNVFGSGTTEE	600			
Db	601 dggegydryhyrsrgnygaltidatketegsytvnrfvtgkalhevtsthalvgnre	660			
Qy	601 DGGCGYDRHYSRGNYGALTIDATKETEGSYTVNRFVTGKALHEVTSTHALVGNE	660			
Db	661 kieyrhsnnqhhagyytktllkavve11gtsd1fkgskfnadafngodgvdtdgndgn	720			
Qy	661 KIEYRHISNNQHHAGCYTKTLLKAVVE11GTSDF1FKGSKFNADAFNGDGDVDTDGN	720			
Db	721 drifggkgdldgnggddfdggkgndfdvfhvkrkgndnditdgdndks	780			
Qy	721 DRIFGGKGDDLDGGNGDDFDGGKGNDLHGGKDDIFVHRKGDGNDITDSGNDKLS	780			
Db	781 fsdnsnlkltfekvhknlyitnskkekvtlqnwfreadfakewpykatzkdekleeiigq	840			
Qy	781 FSDSNPLKDLFEKVHNLYTNSKEKVTQNWFREADFAKEWPYKATKDEKBEIGQ	840			

RESULT 8  
ID R42378 standard; Protein: 924 AA.  
AC R42378;  
DT 19-APR-1994 (first entry)  
DE Recombinant leukotoxin peptide (split) from plasmid pGCH5 .  
SQ 901 DSRNVLVAPTSMLDQSLSSLLQFARGS 926  
SQ 901 DSRNVLVAPTSMLDQSLSSLLQFARGS 926

Query Match 98.6%; Score 6128; DB 10; Length 926;

Query Match



1	MATVIDLESFPKIGAKKILYLIPQNYQVDTEQRERBNNTIA	60	PD	28-OCT-1993.
2	61 qtslgltqtaiglttergivlssapqikllgktagqalgssavisqranktvlgis	120	PF	05-APR-1993; CA0135.
3	61		PR	09-APR-1992; US-8595050.
4	61 QTSLGLTQTAIGLTTERSTIVLSSAPQIDTLKQTKAGQALGSAESTIVQNANKARTVLSIQS	120	PR	04-JUN-1992; US-93424.
5	61 QTSLGLTQTAIGLTTERSTIVLSSAPQIDTLKQTKAGQALGSAESTIVQNANKARTVLSIQS	120	PR	04-JUN-1992; US-93426.
6	121 lsgsviagmdidealqpnnsnqhalaakagleitstieniansvktidegecifqfskl	180	PR	29-MAR-1993; US-038287.
7	121 TIGSVLAGMDDEALQNNQHALAKGLEITSLIENIANSVKTIDEFGEISQTSQSKL	180	PR	29-MAR-1993; US-038288.
8	121 TIGSVLAGMDDEALQNNQHALAKGLEITSLIENIANSVKTIDEFGEISQTSQSKL	180	PA	(USA-) UNIV SASRATCHEWAN.
9	181 qn ikqgtlgdtklnknigldkaglgdqvdivsgllsgataalyladknaстtкvgafel	240	PI	Harland RJ, Pfeiffer CG, Pontarollo RA, Potter AA;
10	181 QNIKGGLQTLGDGLKNGLQGLDVGSLGSATAALYDVKNSTAARKVGAFELA	240	PI	Ricoux C, Theissen M;
11	181 QNIKGGLQTLGDGLKNGLQGLDVGSLGSATAALYDVKNSTAARKVGAFELA	240	DR	WP; 93-1513/34/4.
12	DR N-FSDB; Q51086.		DR	N-FSDB.
13	PT Haemophilus somnis immunogenic proteins used in vaccines -		PT	Haemophilus somnis immunogenic protein used in vaccines -
14	PT selected from haemin-binding protein, haemolysin, LppB and LppB,		PT	selected from haemin-binding protein, haemolysin, LppB and LppB,
15	PT and corresp. DNA		PS	and corresp. DNA
16	PS Disclosure: Fig 11: 119pp; English.		CC	The lppB gene product was expressed in E. coli as a fusion to the
17	CC Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid		CC	pMS11. LppB can be
18	CC pAB352. The lppB gene fragment was taken from pMS11. LppB can be		CC	used in vaccines for preventing or treating H. somnis infections,
19	CC which cause thromboembolic meningo-encephalitis, septicemia, arthritis		CC	and pneumonia in vertebrates.
20	CC See also R42370-86.		CC	
21	SQ Sequence 924 AA;		CC	
22	Query Match 98.4%; Score 6117; DB 8; Length 924;		CC	
23	Best Local Similarity 100.0%; Pred. No. 0.00+00;		CC	
24	Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		CC	
25	Db 1 matvidisfpktgakkilipanygydteggnglqdkvaaseglievqgreenriata	60	CC	
26	Db 1 MATVIDISFPKTGAKKILIPANYGYDTEGGNGLQDKVAEEELGEVQREERNNTIA	60	CC	
27	Db 61 qtslgltqtaiglttergivlssapqidklqlktkagqalgssaisivqnankatkvlgis	120	CC	
28	Db 61 QTSLGLTQTAIGLTTERGIVLSSAPQIDKLQLKTQAGCQSABEIVQNANKATKVLSIQS	120	CC	
29	Db 11 lgsvlqmgmdealqnsnqhalaqgleitstnsliensvktldefegqisqf9sk1	180	CC	
30	Db 11 LGSVLQAGMDEALQNSNQHAKAGLEUTNSLIENSVKTLDFFEGQISQF9SK1	180	CC	
31	Db 121 qnvgnitkavssyilaqrvaqaagsstgpaaliastvslaisplafagiadkfhnaks1	300	CC	
32	Db 121 QNKGIGLGTQDNLQKNTGDKGLDLYISGLSGATAALVADKNNSTAKVYAGFLA	300	CC	
33	Db 121 lgsvlqmgmdealqnsnqhalaqgleitstnsliensvktldefegqisqf9sk1	180	CC	
34	Db 121 LGSVLQAGMDEALQNSNQHAKAGLEUTNSLIENSVKTLDFFEGQISQF9SK1	180	CC	
35	Db 181 qnkglgltgdklknigldkaglgdqvdivsgllsgataalvadknnstakvagfla	240	CC	
36	Db 181 QNKGIGLGTQDNLQKNTGDKGLDLYISGLSGATAALVADKNNSTAKVYAGFLA	240	CC	
37	Db 241 novgnitkavssyilaqrvaqaagsstgpaaliastvslaisplafagiadkfhnaks1	300	CC	
38	Db 241 NOVGNTKAVSSYILAQRVAQAAGSSTGPAALIASTVSLAISPLAFAGIADKFHNAKSL	300	CC	
39	Db 301 esyaerfkkglydgdnallqyqkqamfehaukhnkivewknkhknyfengydarylanqd	420	CC	
40	Db 301 ESYAERFKKGLYDGDNALLQYQKQAMFEHAUKHNKIVEWKNKHKNYFENGYDARYLANQD	420	CC	
41	Db 421 nmkflonlkelqaerviaitqgwdnnigdtagisrlgekylsqkaydafeegkhika	480	CC	
42	Db 421 NMKFLLNLKEIQAERVIAITQGWDNNIGDTAGISRLGEKYLSQLQFAR	480	CC	
43	Db 481 dkvqldqasstfdltovvqrgieldnagnvtktetkittkiakgdendnvfygsgtei	600	CC	
44	Db 481 SKITDQAASSFDLNVQRGIELDNGNVTKTETKITTAKLGEDDDNVFGSCTEI	600	CC	
45	Db 481 dkvqldqasstfdltovvqrgieldnagnvtktetkittkiakgdendnvfygsgtei	600	CC	
46	Db 541 kieyrhsnnqnhagyytktlkaeveeigtshndifgskfrdafngdgrtdndgn	720	CC	
47	Db 541 KIEYRHSNQNHAGYYTKTDLKRAVEEIGTSNDIFGSKENDAFTNGDGVDIDTSDGNDGN	720	CC	
48	Db 541 dkfegydrhygryngaltidatketeqgstsytvrftetgtahertstthtalvgnree	60	CC	
49	Db 541 DKGEGYDRHYGRNGYALTIDATKETEQGSTSYTVRFTETGTAHERTSTTHALVGNREE	60	CC	
50	Db 661 kieyrhsnnqnhagyytktlkaeveeigtshndifgskfrdafngdgrtdndgn	720	CC	
51	Db 661 KIEYRHSNQNHAGYYTKTDLKRAVEEIGTSNDIFGSKENDAFTNGDGVDIDTSDGNDGN	720	CC	
52	Db 721 drfggkgdd1ldggnsoddfidggkgnd1lhggkgddifvrhkgdnditdsdgnaks	80	CC	
53	Db 721 DRFGGGKDD1LDGGNSODDFIDGGKGND1LHGGKGDDIFVHHKGDDIDTSDGNDKLS	80	CC	
54	Db 781 fedsnlkdltfekvkhnlvitskkekvtignwreadfakevpnykatdekeieqq	840	CC	
55	Db 781 FEDSNLKDLTFEKVKHNLVITSKKEKVIGNWREADFAKEVPNTYKATDEKEIEQQ	840	CC	
56	Db 841 ngeritskqvdolliaikngkitcdelskvvdelylkhsksntnsldklissvsaftssn	900	CC	
57	Db 841 NGERITSKQVDOLIAIKNGKITCDELSCKVVDELYLKHSKSNTNSLDKLISSSVSAFTSSN	900	CC	
58	Db 901 dsrnvvaptnmldqsiisslfqar	924	CC	
59	Db 901 DSRNVLPAPTMNLDQSLSSLQFAR	924	CC	
60	RESULT 10		CC	
61	19-APR-1994 (first entry)		CC	
62	Recombinant leukotoxin peptide from plasmid pCR28.		CC	
63	Haemophilus somnis; immunogenic; haemolysin; LppB; LppC;		CC	
64	thromboembolic meningoencephalitis; septicemia; arthritis;		CC	
65	pneumonia; lktA gene; haemin-binding protein; fusion protein.		CC	
66	Pasteurella haemolytica.		CC	
67	WO932123-A.		CC	
68	42385 standard; Protein; 924 AA.		CC	
69	42385.		CC	
70	42385.		CC	
71	42385.		CC	
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RESULT  
ID W03945 standard; Protein: 926 AA.  
AC W03945;  
DT 20-NOV-1996 (first entry)  
DE P. haemolytica truncated leukotoxin (LKT352).  
KW Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH;  
KW fusion protein; immunogen; vaccine; fertility control;  
KW contraceptive; sterilisation; plasmid PAA352.  
OS Pasteurella haemolytica A1 strain Bl22.  
PN W0924675-A1.  
PD 15-AUG-1996.  
PF 24-JAN-1995; CA0009.  
PR US-38447/38.  
PA (UUSA-) UNIV SASKATCHEWAN.  
PI Manus JG, Potter AA;  
WPI: 96-38447/38.  
DR N-PDB: T37179.  
PT Gonadotropin releasing hormone multimer fusion proteins - with  
PT leukotoxin polypeptide for increased immunogenicity, useful in  
PT antifertility vaccine prodn.  
PS Example 1; Fig 3A-3I; 87pp; English.  
CC A truncated leukotoxin (W03945), LKT 352, lacks the cytotoxic  
CC portion of the native protein from Pasteurella haemolytica. It is  
CC the product of plasmid PAA352 which carries a truncated LktA gene  
CC (T37179). A fusion protein (W03942) between Lkt352 and a  
CC gonadotropin releasing hormone tetramer can be expressed in  
CC Escherichia coli. This is useful as a vaccine for fertility  
CC control, partic. immunological sterilisation of domestic or  
CC farm animals.  
Sequence 926 AA:

Query Match 98.4%; Score 6119; DB 19; Length 926;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 924; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 matvidsfptgakkillyipanyqydtapeggqlglvlkaaselgievqreernniata 60  
QY 1 MATVIDLSPPKTAGKKILLYIPQNQYDTEQNGQLDLYKAELGIEVQREERNNIATA 60  
Db 61 qtsigtqtaigtergivisapqdklqktagqalgasaesivqnankaktvlsqis 120  
QY 61 QTSIGTQTAIGTERGIVLSAQIDKLQKTAGQAGSAESIVQNANKAKTVLSQIS 120  
Db 121 ilgsvalagmdldealqgnsnqhalaqaglelttslieniansvktldefgeoisqforsk 180  
QY 121 ILGSVALAGMDLDEALQGNSNQHALAQAGLELTTSLIENIANSVKTLDDEFGEISQFORSK 180  
Db 181 qmikglgtlgdikniggldkaglgldivslgslsgataalvaldnastakkvgagfela 240  
QY 181 QNIKGLGTLGDKLNIGGLDKAGLGLDIVSLGSLSGATAALVALDNASTAKVYAGFELA 240

Db	661	kievrhsnnqhagyyttdtkaveeiigtshndifkgskfnadafngdgvtdngn	720	Db	241	ngvgnitkavssylaqrvaagsstgpvaaliastvsaisplafagiadkfnhaks	1	300
QY	661	KIEVRHSNNQHAGYYTDTKAVEEIIGTSHNDIFGSKFNDAFNGDGVTDNGN	720	QY	241	NOVVGNTKAVSSYILQPVAVGSISSGPVAVIATSVSISPLAFGIDKFNHAKS	1	300
Db	721	drfegkgsddildggngadfdgkgnodllhgkddifvhrgkdgrdiitstdgndkls	780	Db	301	esyaerifklygdgnnlaeaeyrgtqtdasvtaintalaiaiggyrsaaagsviaspia	1	360
QY	721	DRFLFGKGDBDLQNGDDEFDGKGNDLHGSKDDIFVHRKGDGNDITDSGDGNDKLS	780	QY	301	ESYAERERKLGQDGNLJAEXQRGTETIDASTAINTALAIAJAGGSVAAAGSVIASPIA	1	360
Db	781	fsdsnlkdltefekvhnlvitnskekvtqiwfredfakevnyatdkdekkieeqq	840	Db	361	llvsgitgvistilqskqanfehankhakiyveekhnkgnfengyarylanqd	1	420
QY	781	FSDSNLKDLTEFVKVHNVLVITNSKEKVTIONWEREADFAKEVNPYKATKDEKIEEQQ	840	QY	361	LUVSGITGVISTILQSKQAMFEHVANKIHNVKEVNNGKZNPEFNGDARYLANQD	1	420
Db	841	ngeritskvadidaiakngnkitdelkskvvdnyellkhsknvtntsldklissysaftssn	900	Db	421	nmkfllnlinkelqaerviaitcqgqwnniglagisrlsgekhika	1	480
QY	841	NGERITSKVADLIAKGNGKITDELKSKVVDNYELLKHSKNVTNSLDKLISSYSAFTSSN	900	QY	421	NMKFLNLNLKNEQERYVTAITQQWQDNINGDAGRSGVYLGSAYDAFEFGHKIA	1	480
Db	901	dsrnvlvaptsmldqsllsqfar	924	Db	481	dkvqlqdangliidvnsgrktqhtlfirtpiltptehrvqtgkveyitklninrvd	1	540
QY	901	DSRNVLVAPTSMLDQSLLSQFAR	924	QY	481	DKVQLQDSANGLIDVNSGRKTQHFLRTPILTPTEHRRVQTGKVEYITKLNINRVD	1	540
Db	541	swktdgaasssfedlrvqrigieldnqyldagnrtktretktiaklggeddnfvsgsttei	600	Db	541	SWKTDGAASSSFEDLNVORIGIELDNAGNYTKETKILAKLGQDNDNFVGSCTTEI	1	600
QY	541	SWKTDGAASSSFEDLNVORIGIELDNAGNYTKETKILAKLGQDNDNFVGSCTTEI	600	Db	601	dggegydrvhysrgnygaltidatketeggsytvnrfvetghalhevtshtaiygnre	1	660
QY	601	DGEGYDRVHYSRGNYGALTIDATKETEGGSYTVNRFETGHALHEVTSHTAIYGNRE	660	Db	661	kieyrhsnnqhagyytktlkkaveqigtshndifkqskfnadafngqdadvtidgndn	1	720
QY	661	KIEYRHHSNOHHAGYYTKTDLKAVEEITGKTSNDIPGSKPNDAFNGDGVBTIDGNDN	720	Db	721	drlfggddildggdddflogkgnrllogkddifvirkgnrdnditcdgndkis	1	780
QY	721	DRLFGGKDDILDGGNCDDDFIDGGKGNLDLIGKGGDIDFVIRKGNDNDITSDGNDKLS	780	Db	781	fsdsnlkdltfekvhnlvitnskekvtqhtqsfreadfakewpnyatkdkeieeqq	1	840
QY	781	FSDSNLKDLTFEKVKVHNVTNSKKEVKTQHTQSFREADFAKEVNPYKATKDKIEEQQ	840	Db	841	ngeritskvadliakngnkitqhtskvntnsldklissysaftssn	1	900
QY	841	NGERITSKVADLIAKGNGKITQDELSKVVDNYELLKHSKNVTNSLDKLISSYSAFTSSN	900	Db	901	dsrnvlvaptsmldqsllsqfars	1	926
QY	901	DSRNVLVAPTSMLDQSLSLQFARS	926	Db	901	dsrnvlvaptsmldqsllsqfars	1	926
RESULT	12			ID	R34546	standard; Protein: 943 AA.		
ID	R34546;			AC	R34546;			
DT	23-AUG-1993	(first entry)		DT	23-AUG-1993	(first entry)		
DE	Somatostatin-like leukotoxin gene fusion prod.			DE	Somatostatin-like leukotoxin gene fusion prod.			
KW	Vector; LKT 352; flanking; recombinant; antigen; somatostatin;			KW	Vector; LKT 352; flanking; recombinant; antigen; somatostatin;			
KW	gonadotropin releasing hormone; rotavirus viral protein 4;			KW	gonadotropin releasing hormone; rotavirus viral protein 4;			
Key	Synthetic.			Key	Synthetic.			
FT	Location/Qualifiers			FT	Location/Qualifiers			
FT	1..929			FT	1..929			
FT	/note= "recombinant leukotoxin protein"			FT	/note= "recombinant leukotoxin protein"			
FT	peptide			FT	peptide			
FT	/note= "SRIF"			FT	/note= "SRIF"			
PN	W0308290-A.			PN	W0308290-A.			
PD	29-APR-1993			PD	29-APR-1993			
PR	15-OCT-1992; CA0449-			PR	15-OCT-1992; CA0449-			
PR	16-OCT-1991; US-779171.			PR	16-OCT-1991; US-779171.			
PR	14-OCT-1992; US-960932.			PR	14-OCT-1992; US-960932.			
PA	(USA ) UNIV SASRATCHMAN.			PA	(USA ) UNIV SASRATCHMAN.			
PI	Hughes HPA, Potter AA,			PI	Hughes HPA, Potter AA,			
DR	93-152482/18.			DR	93-152482/18.			
DR	N-PSDB; 041231.			DR	N-PSDB; 041231.			
PT	Immunological carrier system with enhanced immunogenicity -			PT	Immunological carrier system with enhanced immunogenicity -			

comprises chimeric protein comprising leuco:toxin peptide or homodotropin fused to antigen esp. somatostatin or gonadotropin releasing hormone.

Example 2: Fig 6; 95pp; English.

Oligonucleotides contg. sequences from bovine somatostatin gene were constructed on a Pharmacia Gene Assembler using standard phosphoramidite chemistry. The oligonucleotides were annealed and ligated into vector pAA352 (contg. the Pateurella haemolytica leukotoxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain JM105. Transformants contg. the oligonucleotide inserts were identified by restriction endonuclease mapping and the recombinant plasmid designated pAA96. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigen alone, i.e. the leukotoxin works as a carrier protein. See also R3545-8.

Sequence 943 AA:

SO:

Score 6107; DB 7; Length 943;

Best Local Similarity 99.8%; Pred. No. 0 00e+00; 1; Mismatches 1; Indels 0; Gaps 0;

Matches 924; Conserved

Db 1 matvidsfpkagkkillyipqnyqydtdeqnglqdvdkaaeelqievreernniata 60

Qy 1 MATVIDSFPKAGKKILYIPQNYQYDTDEQNGLQDVKAEEELQIEVREERNNIATA 60

Db 61 qtslgltqa1gttergivlspaqfkl1gkttkagaalgeasivgnahakatvlsqigs 120

Qy 61 QTSLGLTQTA1GTLTERCIVLSAQPQDQLKQTKTAKGQALGSAEISVONANKRATVLSQIGS 120

Db 121 l1gsvlagmdidealqpnnsndhalakagelitnslieniansvtklddefeqqifqfskl 180

Qy 121 I1GSVLAGMDIDEALQPNNSNDHALAKAGELITNSLIENIANSVTKLDEFEQQIFQFSKL 180

Db 181 qnkgqigtlgdklknnigldkaqlgl1davqslqsgataal1vladknastakkvgagfela 240

Qy 181 QNKKGQIGTLGDKLKNNIGLDKAQLGL1DAVQSLQSGATAALVLADKNASTAKKVGAGFELA 240

Db 241 novvgnitkavssylaqrvvaqslstgrpvvaliestvslaisplapafag1adkfphaks1 300

Qy 241 NQVGVNNTKAVSSYLAQRVVAQSLSTGPVVALIASTVSLAISPLAFAG1ADKFPHAKSL 300

Db 301 esyaerfkklkygdnlalaeyqrgtctidasvtaintalaiaaggysaaagsviaspia 360

Qy 301 ESYAERFKKLKYGDNLALAERQRGTCTIDASVTAINTALAIAAGGYSAAGSVIASPIA 360

Db 361 llvsgitgvistilysqkamtehvankinhkiveweknkhgknyfengdyarylanlqd 420

Qy 361 LLVSGITGVISTILYSQKAMTEHVANKINHKIVEWENKHGKNYFENGDYARLANLQD 420

Db 421 nmkf1lnklnk1qaervviaqgwwnn1qdlag1sr1gkvsckayudafeegkhika 480

Qy 421 NPKFLN1LNKE1QAERVIA1TQQQN1N1D1AG1S1RLGERKVLSGRAYDAFEEGKHKA 480

Db 481 dk1vg1dsang1idvsnsgkak1q11f1pt1ptehzervqtgkveyit1kn1nrvd 540

Qy 481 DK1VQ1DSANG1IDVSNSGKAK1Q11F1PT1PTEHZERVQTGKVEYIT1KN1NRVD 540

Db 541 swkitdgaaassfd1tnvqrq1ielddnagnvtktketk1ia1kgdnnvfgsgttei 600

Qy 541 SWKITDGAAASSFD1TNVQRQ1IELDDNAGNVTKTETK1IA1KGDNNVFGSGTEI 600

Db 601 dggegydrhyrsqnygalt1datketeqsytvorfvetgk1hevtstbtalgnree 660

Qy 601 DGEGYDRHYRSQNYGALT1DATKETEQS1TVORFVETGK1HEVTSTBTALGNREE 660

Db 661 k1eyrhssnnqhagy1ytkt1kveei1gts1hd1f1gskfn1da1ngg1vd1tgndgn 720

Qy 661 K1EYRHSSNNQHAGY1YTKT1KVEEI1GTS1HD1F1GSKFN1DA1NGG1VD1TGNDGN 720

Db 721 dr1fgghgdd1ldgg1dd1f1dg9gknd1lh9gk9gd1f1vhrgk9gd1it1sdgndks 780

Qy 721 DR1FGGHGDD1LDGG1DD1F1DG9GKND1LH9GK9GD1F1VHRGK9GD1IT1SDGNDKS 780

Db 781 f1dsnlkd1tfekvhnh1vitnskekvt1gnwfreadf1akevprnykatkdk1ek1igq 840

Qy 781 F1DSNLKD1TFEKVHN1L1T1NSKEK1V1T1QNFREADE1AKEVPRNYKATKDK1E1IGQ 840

Db 841 ngeritskqvrd1la1gng1ktq1dskvrdnyellkh1knvts1dk1lissysaftssn 900

Qy 841 NGERITSKQVDD1LA1GNG1KTQ1DELSKV1DNYELLKHSKNV1NSLDK1L1SSYSAFTSSN 900

Db 901 dsnrvlvaptmsmlqsls1sqfaras 926

Qy 901 DSRNVLVAP1MSMLQSLSQFARGS 926

RESULT 13

ID R34548 standard; Protein: 951 AA.

AC R34548;

DT 23-AUG-1993 (first entry)

DE Rotavirus VP4-leukotoxin gene fusion prod.

Vector: LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein; SRIF.

Synthetic.

Location/Qualifiers

1..926 /note= "recombinant leukotoxin protein"

927..951 /note= "Rotavirus VP-4"

peptide

FT FT

WO930290-A.

PN PN

PD PD

PR PR

15-OCT-1992; CA0449.

PR PR

16-OCT-1991; US-779171.

PA PA

(U.S.A.) UNIV SASKATCHEWAN.

PI PI

Hughes HPA, Potter AA, Redmond MJ;

DR DR

N-PSDB; Q41322.

PT Immunological carrier system with enhanced immunogenicity - comprises chimeric protein fused to antigen esp. somatostatin or homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone

Example 2; Fig 9; 95pp; English.

Oligonucleotides contg. sequences from bovine Rotavirus viral protein 4 (VP-4) gene were constructed on a Pharmacia Gene Assembler using standard phosphoramide chemistry. The oligonucleotides were annealed and ligated into vector pAA52 (contg. the Pateurella heamolyticus leuko-toxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain MH3000. Transformants contg. the oligonucleotide inserts were identified by restriction endonuclease mapping and the recombinant plasmid designated pAA51. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigen alone, i.e. the leukotoxin works as a carrier protein. See also R34545-7.

Sequence 951 AA;

Query Match 98.1%; Score 6100; DB 7; Length 951;

Best Local Similarity 99.7%; Pred. No. 0.00e+00; Matches 923; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 matvidsfptkgakk1lyipqnyqydtteqnglqdvdkaaeelqievqgreenriata 60

Qy 1 MATVIDSFPTKGAKK1LYIPQNYQYDTTEQNGLQDVKAEEELQIEVQGREENRIATA 60

Db 61 qtslgltqa1gttergivlspaqfkl1gkttkagaalgeasivgnahakatvlsqigs 120

Qy 61 QTSLGLTQTA1GTLTERCIVLSAQPQDQLKQTKTAKGQALGSAEISVONANKRATVLSQIGS 120

Db 121 l1gsvlagmdidealqpnnsndhalakagelitnslieniansvtklddefeqqifqfskl 180

Qy 121 I1GSVLAGMDIDEALQPNNSNDHALAKAGELITNSLIENIANSVTKLDEFEQQIFQFSKL 180

Db 181 qnkgqigtlgdklknnigldkaqlgl1davqslqsgataal1vladknastakkvgagfela 240

Qy 181 QNKKGQIGTLGDKLKNNIGLDKAQLGL1DAVQSLQSGATAALVLADKNASTAKKVGAGFELA 240

Db 241 novvgnitkavssylaqrvvaqslstgrpvvaliestvslaisplapafag1adkfphaks1 300

Qy 241 NQVGVNNTKAVSSYLAQRVVAQSLSTGPVVALIASTVSLAISPLAFAG1ADKFPHAKSL 300

Db 301 esyaerfkklkygdnlalaeyqrgtctidasvtaintalaiaaggysaaagsviaspia 360

Qy 301 ESYAERFKKLKYGDNLALAERQRGTCTIDASVTAINTALAIAAGGYSAAGSVIASPIA 360

Db 361 llvsgitgvistilysqkamtehvankinhkiveweknkhgknyfengdyarylanlqd 420

Qy 361 LLVSGITGVISTILYSQKAMTEHVANKINHKIVEWENKHGKNYFENGDYARLANLQD 420

Db 421 nmkf1lnklnk1qaervviaqgwwnn1qdlag1sr1gkvsckayudafeegkhika 480

Qy 421 NPKFLN1LNKE1QAERVIA1TQQQN1N1D1AG1S1RLGERKVLSGRAYDAFEEGKHKA 480

Db 481 dk1vg1dsang1idvsnsgkak1q11f1pt1ptehzervqtgkveyit1kn1nrvd 540

Qy 481 DK1VQ1DSANG1IDVSNSGKAK1Q11F1PT1PTEHZERVQTGKVEYIT1KN1NRVD 540

Db 541 swkitdgaaassfd1tnvqrq1ielddnagnvtktketk1ia1kgdnnvfgsgttei 600

Qy 541 SWKITDGAAASSFD1TNVQRQ1IELDDNAGNVTKTETK1IA1KGDNNVFGSGTEI 600

Db 601 dggegydrhyrsqnygalt1datketeqsytvorfvetgk1hevtstbtalgnree 660

Qy 601 DGEGYDRHYRSQNYGALT1DATKETEQS1TVORFVETGK1HEVTSTBTALGNREE 660

Db 661 k1eyrhssnnqhagy1ytkt1kveei1gts1hd1f1gskfn1da1ngg1vd1tgndgn 720

Qy 661 K1EYRHSSNNQHAGY1YTKT1KVEEI1GTS1HD1F1GSKFN1DA1NGG1VD1TGNDGN 720

Db 721 dr1fgghgdd1ldgg1dd1f1dg9gknd1lh9gk9gd1f1vhrgk9gd1it1sdgndks 780

Qy 721 DR1FGGHGDD1LDGG1DD1F1DG9GKND1LH9GK9GD1F1VHRGK9GD1IT1SDGNDKS 780

Db 781 f1dsnlkd1tfekvhnh1vitnskekvt1gnwfreadf1akevprnykatkdk1ek1igq 840

Qy 781 F1DSNLKD1TFEKVHN1L1T1NSKEK1V1T1QNFREADE1AKEVPRNYKATKDK1E1IGQ 840

Qy	181	QNIGLJGTLGDKLNKGGLDRAGLGDVSSLLSGATAALVLADRNASTAKVGAGFELA	240	CC leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. CC LKT 352 and preI. antigenic fragments of it, can be used in CC vaccines to protect cattle from respiratory diseases. They can also CC be used to produce antibodies for immunoaffinity purification of CC further proteins. [Fig. contng. sequence v. poor]. CC See also R10890, R10909, R10910 and Q10783.
Db	241	novvgnitkavssylaqrvaaqslstgprvaaliastvsiaiplafagladkfphaks1	300	CC
Db	241	NQVYGNITKAVSSYLQAQRVAATGLSSGPYAAIATSVLAISPLAFAGIADKENHAKSL	300	CC
Db	301	esyafkfk19dgdn11aeyrgtgtidavtialaiaggysaaaagsviaspia	360	CC
Qy	301	ESYAERFKKLGGDNLIAEFGTGTIDAVTAINTALAAIAGGSAAAAGSVIASPIA	360	CC
Db	361	livsgitgvistilgyksqanfehvankihnkiveweknnhgknypengydarylanlqd	420	CC
Qy	361	LIVSGITGVISTILGYKSQANFEHVANKIHNKIVEWENNGKNTFENGTDARYLANLQD	420	CC
Db	421	nnkf1lnlnklaervviaitcqgwankigdlagsrlgekvlskayvdafeeghika	480	CC
Qy	421	NPKFLNLNKEAQAEVIAITQQQWNNNIGLAGISRLGEKVLSKAYDAFEEGHKHA	480	CC
Db	481	dklvqldangs1dvsnsgaktqhiflfrpltpg Lehrervtqskyevitklninrvd	540	CC
Qy	481	DKLVQLDSANG1DVNSNGAKTQH1LFRPLTPG Lehrervtqskyevitklninrvd	540	CC
Db	541	swkitdgaasssfldltvvqr1gieldnagnvktktetkiklgkgdnnvfgsgttei	600	CC
Qy	541	SWKITDGAASSSFDLTNVVRQ1GILDAGNVTGALTTKETKIKLGKGDDNVFGSGTEI	600	CC
Db	601	dgegeydrvhysrgnygaltidatketeggytvnrsvetgk alhevsttthalvgnree	660	CC
Qy	601	DGEYDGRVHYSGRNYGALTIDATKETEQQSYTVNRVEIGKALHEVTSHTALVGNREE	660	CC
Db	661	kieyrhsnnqhhagyykdtklaveel1gtshndifkgsfnadfrggdytidgnndn	720	CC
Qy	661	KEYRHNNQHHAGYYKDTLKAVEEL1GTSHNDIFGSKSENDAFNGGDTIDGNDGN	720	CC
Db	721	drlfqgkqddildgngnddfldgqkandllbhgkgqdifvhrgkgdndiitdsdgnkls	780	CC
Qy	721	DRLFGGKQDDILDGNGDDFTIGGKNDLHGGKQDDIFHRKGKDNDIITDSDGNKLS	780	CC
Db	781	fdsn1kdltfekvkmlvitskekvtgvfreadfakepnykatdekkieeqg	840	CC
Qy	781	FSDSN1KDLTFEKVKMLVITSKEKVTGVFREADFAKEPNYKATDEKIEBIIQG	840	CC
Db	841	ngeritskqvddlia1gngk1tqdelksvvnylellkhskntnsidklissvsaftssn	900	CC
Qy	841	NGERITSKQVDLIA1GNGK1TQDELKS VVNYLELLKHSKNTNSLDDKLISSVSAFTSSN	900	CC
Db	901	dsrnvlvaptsmldqss1lqfargs	926	CC
Qy	901	DSRNVLVAPTSMDQSSLQFARGS	926	CC
RESULT	14			
ID	R10889	standard; Protein: 924 AA.		
AC	R10889			
DT	11-APR-1991	(first entry)		
DE	Leukotoxin 352 encoded by Plasmid pAA352.			
KW	Lkt; vaccine; antigen; respiratory disease; shipping fever pneumonia.			
OS	Pasteurella haemolytica A1 strain B122.			
PN	CA201433-A.			
PD	07-OCT-1990.			
PF	07-APR-1989; US SAWATCHHWA.			
PA	Acres SD, Babuuk LA, Potter AA, Lawman MJP;			
PI	WPI: 91-00097/01.			
DR	N-PSDB; Q10272.			
PT	Pasteurella haemolytica proteins and genes - used for producing vaccines to protect animals esp. cattle from respiratory diseases e.g. pneumonia.			
PR	Claim 13; Fig 5; 87PP; English.			
PS	Plasmid pAA352 is derived from pAA14, a clone isolated from a genomic library of P. haemolytica. The protein, designated "new			
CC	839 ngeritskqvddlia1gngk1tqdelks vvnylellkhskntnsidklissvsaftssn			
CC	841 NGERITSKQVDLIA1GNGK1TODELSKVNTNSLDDKLISSVSAFTSSN			
Db	899 dsrnvlvaptsmldqss1lqfargs			

Qy	901	DSRNLYVAPTSMDQSLSSTQFARGG	926	
RESULT	15			
ID	W13866	standard; Protein;	1098 AA.	
AC	W13866			
DE	12-MAY-1997	(first entry)		
DE	Chimeric protein #1.			
RTX	cytokine; immunogen; chimeric protein; cytokine; vaccine;			
KW	interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia;			
KW	Pasteurella haemolytica; Lkr352; respiratory disease; shipping fever;			
KW	fibrinous pneumonia; cattle; therapy.			
OS	Synthetic.			
PN	US554107-A.			
PD	14-JAN-1997.			
PF	22-AUG-1990.	571301.		
PR	22-AUG-1990.	US-571301.		
PR	16-OCT-1994.	US-77715.		
PR	20-DEC-1993.	US-170126.		
PA	(CIBA ) CIBA BRITISH CANADA LTD.			
PA	(U.S.A.) CIBA SASKATCHEWAN.			
Campos M.	Hughes HPA, Potter A;			
PI	DR WPI; 97-09529/09.			
DR	N-PSDB; 16032.			
PT	Immunogenic chimeric proteins comprising cytokine linked to RTX toxin useful in vaccines, esp. against shipping fever in cattle.			
PS	Claim 10; Column 25-32; 56pp; English.			
CC	W13866 and W13867 represent immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine interleukin-2 (IL-2) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from IL-2 and gamma interferon (gamma IFN), linked to at least one RTX toxin epitope (preferably the sequence shown in W13865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially Lkr352. The chimeric proteins can be used for the production of vaccines against respiratory diseases such as pneumonia, particularly the fibrinous pneumonia caused by P. haemolytica, including shipping fever in cattle.			
SQ	Sequence 1098 AA:			
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	Best Local Similarity 100.0%; Pred. No. 0.00e+00;			
	Matches 916; Conservative 0; Nismatches 0; Indels 0; Gaps 0;			
Db	183	ktgakkiiyipqnyqydteqnglqlqdivkvaeeelqiegvergreenriataqtsgtqta	242	
Qy	11	KTGAKKIIYIPQNYQDTEQNGLQLDKRAEEELGIEQREERNNTIATAQTSGTQTA	70	
Db	243	iglttergivlspaqidklqlqtkqgalgsaesiivqnaankakvlsgisilsvlagmd	302	
Qy	71	IGLTTERGIVLSPAQIDKLQLDKRAEEELGIEQREERNNTIATAQTSGTQTA	130	
Db	303	idealqnnsnqhalaqakileitnsnieniansvtlddefeqisqfsgsklnikqigtg	362	
Qy	131	LDEALQNNSNQHALAQAKILEITNSNLENIASTVTLDEGEQLSQFGSKLNQKGLGTG	190	
Db	363	dklknnigglidkaglgldvisqlsgataalvadknastakkrqagfelangrygnitka	422	
Qy	191	DKLKNNIGGLDAGLGLDVISQLSGATAALVADKNASTAKKRQAGFELANGYGNITKA	250	
Db	423	vssyilaqrvaaqlsystgvaaialstvslaisplafaciadkfnhakslesyaerfkk	482	
Qy	251	VSSYILAQRVAAQLSYSTGPVAAILSTVSLAISPLAFACIADKFNHAKSLAESYERFKK	310	
Db	483	gydgdanllaeqrgtgtdasvtaataiagovsaaaagsiaspiallysgitav	542	
Qy	311	GYGDGNLLAEQRTGTTIDASVTAATAIAGOVSAAGGSVIASTALLSGITGV	370	
Db	543	stilqskqamfehvanikhnvewekvhnhkgnyfengydarlylanlqdnmkfllnlk	602	
	Qy	371	STILQSKQAMFEHVANKIHNVWEKEVKNHKGNYFENGYDARYLANLQDNMKFLNLNK	430
	Db	603	elgaervlaiteqgdndlgdagisrlqekylsgkayda feegkhikadk.lvgldsan	662
	Qy	431	ELQAERVTAITQQWDNNIGLAGISRGKAYDAGEGHKADLVLQDSL	490
	Db	663	giidvsnsgaktkghiflfrptlptgtrherqvtgkyeyitklninrvdsrktdgaa	722
	Qy	491	GILDVSNSGAKTKHIFLFRPTLPTGTRHERQVTGKYEYITKLNINRVDSRKTDGAA	550
	Db	723	stfdltnvqrqigieldnagntktktkiaqlgeodnfvfgsgttedggeydrh	782
	Qy	551	STFDLTVNVRQIGIELDNAGNTKTKTKIAQLGEODNVEFGSGTEIDGEGIDR VH	610
	Db	783	ysrgnygatidatketeqsgsvnrfvngrekleyrhsnq	842
	Qy	611	YSRGNYGATIDATKETEQSGSVNRFVNGREKIEYRISNNQ	670
	Db	843	hhagyytkdtlkaveei1gtsndifgkskndafngggdytdidngdnrlfkgqdd	902
	Qy	671	HHAGYYTKDTLKAVEEITGGSHDIFPGSKFNDAFNGDGTIDGNDNLFGGGDD	730
	Db	903	ildggngdffdggkgndllhgkgddifhrkgndoditsdngndklsfedsn1kdlt	962
	Qy	731	ILDGGNGDFFDGKGNDLHGSKGDDIFHRKGDNIDTSDGNDKLSFSDSN1KDLT	790
	Db	963	fervhkhnlivitnkkelvtnqwfredfakvepnyratdkdkiehlgndneritskqv	1022
	Qy	791	FERVKHNLIVITNSKKERYVIQNWREADAKEPVNPYKATDEKIEIGQNGERITSKQV	850
	Db	1023	ddiakengkgkitgdelkskvdnvylellkskavnts1dklissavaftssndsrnlyapt	1082
	Qy	851	DDIJAKGNGKITODELSKVVDNLYELLKHSRNVINSDDKLISSVSRAFTSSNDSRNVLVAPT	910
	Db	1083	smldqslsllsqfargs	1098
	Qy	911	SMLDQSLSSLSLQPARGS	926
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#accession A4834  
#molecule-type DNA  
##residues 1-956 ##label BUR  
##experimental\_source\_isolate 3714  
##note sequence extracted from NCBI backbone (NCBIN:104212; NCBIP:104211)  
COMMENT This organism causes acute fatal septicemia in young pigs.  
FUNCTION #description attacks cell membranes and causes cell lysis  
CLASSIFICATION superfamily hemolysin A; hemolysin A homology  
KEYWORDS calcium binding; cytolysis; exotoxin; hemolysin; lipoprotein;  
tandem repeat  
FEATURE #domain hemolysin A homology #label HLYA\\  
243-787 #region 9-residue repeats\\  
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782-790 #region repeat\\  
793-801 #binding\_site palmitate (Lys) (covalent) #status  
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SUMMARY Query Match 67.5% Score 4198; DB 1; Length 956;  
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Db 103 FTDRGIVLAPOLKNUKKPKPKNPQKNTLGASSISONKANTVLIGSLSVLSGVNL 162  
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Qy 371 STILOYSKQAMFEHANKYHDTIVEWEK-HNKQYFEQYDSRHLADODNMKELINLNK 430  
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#ashA protein: Cytolysin II; RTX-toxin II  
#formal name: *Actinobacillus suis*  
#sequence\_change 31-Dec-1993 #sequence\_revision 08-Nov-1996 #text\_change  
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CESSIONS  
#authors Burrows, L.L.; Lo, R.Y.  
#title Insect Immun (1992) 60:2166-2173  
#molecular characterization of an RTX toxin determinant from  
#title 551 STED1INVQRIIGELDNQGAVNTTKEKIIAKJEGDDNVYFGSGTTEIDGGEYDYDRH 610  
#title 581 SSVDEFTNVQYREAVKFDDAGNIESKDTKIANLGAGDNVFGSSTTYDGGDGHDRYH 640  
#title 491 GIIDVNSNSGRAKTQHFLFRPLTGPTEERVOTGKYEITKINNRDSWKTGDAIS 550  
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#title 371 STILOYSKQAMFEHANKYHDTIVEWEK-HNKQYFEQYDSRHLADODNMKELINLNK 430  
#title 462 ELQAERVVAITQQRMDNQICDAAISRRPDKISSKGKAYDAFECQHQSYDSSVYOLDNKN 521  
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Qy 722 RLFGGKDDILDGGNGDDFIDGKGNDLHGKGDDIFVHRKGDGND 768

RESULT 6 S51784 #type complete toxin III - Actinobacillus pleuropneumoniae (serotype 2)

ENTRY RTX-toxin IIIA (ApXTIIA)

ALTERNATE\_NAMES # formal name Actinobacillus pleuropneumoniae

ORGANISM 14-Jul-1995 #sequence\_revision 15-Nov-1996 #text\_change 06-Dec-1996

ACCESSIONS S51783

authors Chang, Y.F.; Shi, J.; Ma, D.P.; Shin, S.J.; Lein, D.H.

JOURNAL DNA Cell Biol. (1993) 12:351-362

Molecular analysis of the Actinobacillus pleuropneumoniae RTX toxin-III gene cluster.

accession S51784

#status preliminary

#molecule\_type DNA

#residues 1-1049 #label CHA

#cross-references EMBL:Li2145; PID:9470685

COMMENT This organism causes porcine pleuropneumonia.

GENETICS #gene apXTIIA

FUNCTION lyses lung macrophages

CLASSIFICATION #superfamily hemolysin A; hemolysin A homology

KEYWORDS calcium binding; cytolysis; exotoxin; lipoprotein; tandem repeat

FEATURE 254-803 #domain hemolysin A homology #label HLYA\

761-861 #region 9-residue repeats (G-G-X-G-[DN]-D-X-[LVYIF]-X)\

735-743 #region repeat #status atypical\

744-753 #region repeat #status atypical\

753-761 #region repeat\

762-770 #region repeat\

771-779 #region repeat\

780-788 #region repeat\

789-797 #region repeat\

798-806 #region repeat\

807-825 #region repeat\

817-824 #region repeat\

826-834 #region repeat\

835-843 #region repeat\

844-852 #region repeat\

853-861 #region repeat\

571-702 #binding-site palmittate (Lys) (covalent) #status Predicted

SUMMARY #length 1049 #molecular\_weight 112491 #checksum 8555

Query Match 41-38: Score 2566; DB:1; Length 1049;

Best Local Similarity 52.2%; Pred. No. 0.0e+00;

Matches 401; Conserved 177; Mismatches 167; Indels 23; Gaps 20;

Db 55 GNKLVLVIP-K FYDSVGNGFFDLVKAEEGLQIVKYVNRELEVAKSLGTADQFLGL 112

Qy 14 KAKLILYIPOQNYQDTEQKQHAAKQLEQVQERQNIATAQSLTQTAIGL 73

Db 113 TERGLTLPAPOLDQFLQKHSKSNVYGSSTDAYSRLAKSQTTIINGQSYSLGTVLAGINL 172

Qy 74 TERTGIVLSSAPQDQLQK-TRAGQALGSAE-TVQIANAKAKTVLSGIQSISLGMDL 131

Db 173 NEAIISSGSEELFAEAGVSLASELVSNIAKSTTIDAFTTQIQNQG-KLAENAKGLGGVG 231

Qy 132 DEALQNSNQIAKAGLETLNSLIENTANSVKTIDFEGQISQGSKL-QNIRGLTG 190

Db 232 RQLONISGSALSKTGQGLDISSLLSGVTSFALKNKNSTSKVYAGFELSNQVIGGIT 291

Qy 191 DKLNKIG-1DKAGLGLDVTSLSGQATAVLADKNASTAKKVYAGFELSNQVIGGIT 248

Db 292 KAVSSYLLAQQRAGLSTGPAAUAIASSISLAISPLAFLRVADNFNRSEIGEFAERFK 351

Qy 249 KAVSSYLLAQRYVAAGLSSTGPVAAIASVSLAISPLAFAGIAKDNFHAKSLEYAERFK 308

Db 352 KLGYDGDKLLSEFYHEAGTIDASITTSALAACTAAAGTAAASAGLVGAPITLIVTGITG 411

Qy 309 KLGYDGDNLIAEYORGTTGIDASITTAATTAAGTAAAGSVIASPIALIVSGITG 368

Db 412 LISGLEFSKOPMELDHVASKIGNKTDIEWKK-YGKNYFFENGYDARHKAFLEDFSLISSE 470

Qy 369 VIStLQYXSKOAMPFHVANKTHKIVEWNNHGKNYFENGYDARYLANQDNMKFLNL 428

Db 471 NKYETERAVLITOQRWDXEYIGELLAGITGKDKLSSKRAYDVYDFOEQGKLEKEPPDDFSKV 530

Qy 429 NKEGAERTIAITQDWNNGDAGISLGEKVLSKRAYDVDAFEEGRHI--RADKL--v 484

Db 531 VEDPTKGDELDISNS-OTSPL-LKVTPLUTPGTESRERTQTGKYEYTKLVVGGKDWWV 588

Qy 485 QLDSANGIDYDVSNEGKAKTQHILFRTPLTPGEHRRQVYDGTQYEXYTKLNINIRVDSPKI 544

Db 589 NGVRDKGAYDVTNLQHATHIS-SSVARQEYEVYRVLVSHLGNQNDKVYLAASAEATHAG 647

Qy 545 TDGAA-SSFDLTNVYVORIGLIEDNAGNVTKTETKILAKLGEGBDDNVEFGSGTEIDGG 603

Db 648 EGHDVVYYPDKTDGILVIGDTKATEQGRYSVTRELSGATKILREVIKNQYAVGKREEL 707

Qy 604 EGYDRVHYSGRNQGALTIAKETEQGSYTVNR-FVETGKALREVTSHTALVGNREEMI 662

Db 708 EYRDYELTQSNSNSNIKAHDDELHSWEETI-GSNQRFDEKGSKFRDIFHGADDDLLNGDND 766

Qy 663 EYRHSN-NOH-HAGYXTKTLKAVEEITGSHNDIFGSKENDAFNGGCVDTIDGNDN 720

Db 767 DILYGDKGNDDELRGDNGNDOLYGEGBDDKLLGGNNN-YL-SCGDGN 812

Qy 7221 DRLLFGKGDDILDGGNGDFFIDGGKNDLHKGKDDIFVHRKGDGND 768

RESULT 7 LEECA #type complete

ENTRY TITLE hemolysin A - Escherichia coli

ORGANISM #formal\_name Escherichia coli

DATE 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 20-Mar-1988

ACCESSIONS A24433; I41280

REFERENCE A24433

authors Feimilee, T.; Pellett, S.; Welch, R.A.

journal J. Bacteriol. (1985) 163:94-105

title Nucleotide sequence of an Escherichia coli chromosomal hemolysin

#cross-references MULD:855334404

#accession A24433

#molecule\_type DNA

#residues 1-1023 #label FEL

REFERENCE A55387

authors Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.

journal Science (1994) 266:1982-1986

title Fatty acylation of two internal lysine residues required for the toxic activity of Escherichia coli hemolysin.

#contents annotation; lysine palmitoylation

#note lysine modification is performed by the hlyC gene product

REFERENCE I41280

authors Haertlein, M.; Schiessl, S.; Wagner, W.; Redest, U.; Kreft, J.; Goebel, W.

journal J. Cell Biol. (1993) 22:87-97

title Transport of hemolysin by Escherichia coli.

#accession I41280

##status translated from GB/EMBL/DBJ

#molecule\_type DNA

#residues 1-'T', 3,'V',5,'T',7-44 #label RES

##cross-references GB: M29173; PID:9146337; PID:9146338

GENETICS

#gene hiYA

FUNCTION #description attacks blood cell membranes and causes cell lysis

CLASSIFICATION #superfamily hemolysin A; hemolysin A homology  
KEYWORDS calcium binding; cytolsis; exotoxin; hemolysis; lipoprotein;  
tandem repeat

FEATURE #domain hemolysin A homology #label HLYA\\  
723-851 #region 9-residue repeats [G-X-G-[DN]-D-X-[LVYF]-X]\\  
723-731 #region repeat #status atypical\\  
732-740 #region repeat #status atypical\\  
741-749 #region repeat\\  
750-758 #region repeat\\  
759-767 #region repeat\\  
768-776 #region repeat\\  
777-785 #region repeat\\  
786-794 #region repeat\\  
795-803 #region repeat\\  
806-814 #region repeat #status atypical\\  
816-824 #region repeat\\  
825-833 #region repeat\\  
834-842 #region repeat\\  
843-851 #region repeat\\  
563-689 #binding site palmitate (Lys) (covalent) #status  
experimental #length 1023 #molecular-weight 109866 #checksum 127

SUMMARY #length 1023 #molecular-weight 109866 #checksum 127

Query Match 38.6%; Score 2398; DB 1; Length 1023;  
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Matches 381; Conservative 184; Mismatches 178; Indels 30; Gaps 23;

Db 43 RNAGNRILLIPKDYK-G-QGSSSLNDLVRPADELGIEYOYDEKNTATIKQVFGTAEKL 99  
Qy 11 KTGAKKILIPQNYQYDTEQNGLQDLVKAAELGIEVOREERNNIATAQSLGTIQA 70

Db 100 IGLTERGVTFAPOLDKLQKQAGNKLGGSAENIDNLKGAGSVLSTQNFGTAISS 159  
Qy 71 IGLTERGVIVLSAPQDKLQR-TRCAQALG-SAESIVONANKAKTVLGSQISLGSVLAG 128

Db 160 MKDELIIKKQSGGNVSSSELAKESTELINOLVDT AASLNVNNSFSQQLNKLGSVLSNT 218  
Qy 129 MDLDEAL- -QNS-N-QHA -LAKAGLELTNSLIENTANSVTKLDFEQSQSFQSKLQNI 183

Db 219 KHLNGVGNIKQNLNPNDNIGLDTVSGILSAISASFNSNADDTGTRAAAGVELTTKV 278  
Qy 184 KGLGTGDKLKNIGGLDKGAGLDDVSGLSSATAVLAQDKNASTAKVGAFFELANQV 243

Db 279 LGNGKGKISQYIQAQRAAOGLSTSAAAAGLITASVYVTLAISPLSFLSIADKEKRANKIEY 338  
Qy 244 VGNITKAVSSYTLAQVAAGLSTGPGVAALLASTVSLAISPLAFAGIADEFNHAKSLEY 303

Db 339 SQRFKKLGDDSLAFAHKPTGADASLSTRISTYLAVSSGISAANTSLVGAPVSLV 398  
Qy 304 AERFKLGDDNLIAEYQRTGTDASVTAINTALAAITAGGVAAAANGSVIASPALLY 363

Db 399 GAVFTKIGSLIDEASKOMFEVASKMADVIAWEKK-HGKNYFENGDYDARHAAFLDENFK 457  
Qy 364 SGITGVISTLQQYSKOMFEHVANKTHNKIVWEKNNHGKNYFENGDYDARYLANLODMNK 423

Db 458 ILSOXNKKEYSVERSLJITOHDWTLJIGELAGTTRNGDKTLGSKSVIDYYEGKRLEKKPD 517  
Qy 424 FLLNLNLKELQARVIAITQODNNIGLASICRGEKVSAYDAFEKGKH--KAD 481

Db 518 EFOQVFDPLKGNIIDS-KSTL-LKFVTPPLTGEERBRROSGKYEITELLVKGV 575  
Qy 482 KIV-QL-DSANGIITDYSNSGAKTOHLLFRPLPTEERVQTKYEITKINIRV 539

Db 576 DKWTVKGQDKGSVSYDVSNLQHASY---GN-NOYREIRESHLGDDKVFSLAGSA 629  
Qy 540 DSWKIDGAA-STSEDLTNVQRIGHTDNGNVTKTKEKIAKUGEDDNVFTGSHT 598

Db 630 NIYAGKGDVYVYDKDDTGILTDTKATEAGNYTTRVGGDKVYQEUVKEQFYSVCK 689  
Qy 599 EIDGEGCYDRYHSRNQYGAUTIDATKETEGGSYVNRFVETG-KALHEVTSHTALVGN 657

Db 690 RTEKTOYRSYEFTHINGKNLTEDNLYSVEBLIGTRADKEFGSKFADIFHAGDDHIE 749

Qy 658 REEKTEYRHSNNOHAG-YXT-KOTLKAVEEIICTSNHNDFKGSKFNDAEFGDCVDTID 715  
Db 750 GNDGNDRLXKDGNPDTLSGGNGDDOYLGGGNDKLIGGAGN-YLN-GDGDD 800  
Qy 716 GNDGNDRLFEGKGDIDLGNGDDFIDGGKNDLHGGKGDDFVHRKGDGND 768

RESULT 8

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TITLE hemolysin A - Escherichia coli Plasmid phly152  
ORGANISM #formal name Escherichia coli  
DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change  
30-May-1997

ACCESSIONS S10056  
REFERENCE S07209  
#authors Hess, J.; Wels, W.; Vogel, M.; Goebel, W.  
JOURNAL FEMS Microbiol. Lett. (1986); 34:1-11  
#title Nucleotide sequence of a plasmid encoded hemolysin determinant and its comparison with a corresponding chromosomal hemolysin sequence.

#accession S10056  
#status preliminary  
#molecule\_type DNA  
#residues 1-1024 #label HES  
#cross-references EMBL: M14107

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#length 1024 #molecular\_weight 110154 #checksum 94113

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Best Local Similarity 48.5%; Pred. No. 0.0e+00;  
Matches 376; Conservative 188; Mismatches 180; Indels 29; Gaps 22;

Db 43 RNAGNRILLIPKDYK-G-QGSSSLNDLVRPADELGIEYOYDEKNTATIKQVFGTAEKL 99  
Qy 11 KTGAKKILIPQNYQDTEQNGLQDLVKAAELGIEVOREERNNIATAQSLGTIQA 70

Db 160 MKDELIIKKQSGGNVSSSELAKESTELINOLVDT AASLNVNNSFSQQLNKLGSVLSNT 218  
Qy 129 MDLDEAL- -QNS-N-QHA -LAKAGLELTNSLIENTANSVTKLDFEQSQSFQSKLQNI 183

Db 219 KHLNGVGNIKQNLNPNDNIGLDTVSGILSAISASFNSNADDTGTRAAAGVELTTKV 278  
Qy 184 KGLGTGDKLKNIGGLDKGAGLDDVSGLSSATAVLAQDKNASTAKVGAFFELANQV 128

Db 260 MKDELIIKKQSGGNVSSSELAKESTELINOLVDT AASLNVNNSFSQQLNKLGSVLSNT 219  
Qy 129 MDLDEAL- -QNS-N-QHA -LAKAGLELTNSLIENTANSVTKLDFEQSQSFQSKLQNI 183

Db 220 KHLNGVGNIKQNLNPNDNIGLDTVSGILSAISASFNSNADDTGTRAAAGVELTTKV 279  
Qy 184 KGLGTGDKLKNIGGLDKGAGLDDVSGLSSATAVLAQDKNASTAKVGAFFELANQV 128

Db 280 LGNGKGKISQYIQAQRAAOGLSTSAAAAGLITASVYVTLAISPLSFLSIADKEKRANKIEY 339  
Qy 244 VGNITKAVSSYTLAQVAAGLSTGPGVAALLASTVSLAISPLAFAGIADEFNHAKSLEY 303

Db 340 SQRFKLGDDSLAFAHKPTGADASLSTRISTYLAVSSGISAANTSLVGAPVSLV 399  
Qy 304 AERFKLGDDNLIAEYQRTGTDASVTAINTALAAITAGGVAAAANGSVIASPALLY 363

Db 400 GAVFTKIGSLIDEASKOMFEVASKMADVIAWEKK-HGKNYFENGDYDARHAAFLDENFK 458  
Qy 364 SGITGVISTLQQYSKOMFEHVANKTHNKIVWEKNNHGKNYFENGDYDARYLANLODMNK 423

Db 459 ILSONKEYSVERSLJITOHDWTLJIGELAGTTRNGDKTLGSKSVIDYYEGKRLEKKPD 518  
Qy 424 FLLNLNLKELQARVIAITQODNNIGLASICRGEKVSAYDAFEKGKH--KAD 481

Db 518 EFOQVFDPLKGNIIDS-KSTL-LKFVTPPLTGEERBRROSGKYEITELLVKGV 575  
Qy 482 KIV-QL-DSANGIITDYSNSGAKTOHLLFRPLPTEERVQTKYEITKINIRV 539

Db 576 DKWTVKGQDKGSVSYDVSNLQHASY---GN-NOYREIRESHLGDDKVFSLAGSA 629  
Qy 540 DSWKIDGAA-STSEDLTNVQRIGHTDNGNVTKTKEKIAKUGEDDNVFTGSHT 598

Db 630 NIYAGKGDVYVYDKDDTGILTDTKATEAGNYTTRVGGDKVYQEUVKEQFYSVCK 689  
Qy 599 EIDGEGCYDRYHSRNQYGAUTIDATKETEGGSYVNRFVETG-KALHEVTSHTALVGN 657

Db 690 RTEKTOYRSYEFTHINGKNLTEDNLYSVEBLIGTRADKEFGSKFADIFHAGDDHIE 749



REFERENCE	#authors	Tasconi, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa, I.; Rodriguez-Ferri, E.F.
#journal	Mol. Microbiol.	The RTX haemolysins ApX1 and ApXII are major virulence factors of the swine pathogen Actinobacillus pleuropneumoniae: evidence from mutational analysis.
#title		
S66731		
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#molecule-type DNA	#residues 604-685 #label TAS	COMMENT: This organism causes porcine pleuropneumonia.
GENETICS #gene apXA	FUNCTION #description attacks blood cell membranes and causes cell lysis	
CLASSIFICATION #superfamily hemolysin A: homology	KEYWORDS #domain hemolysin A homology #label HYA\	
FEATURE 243-789	721-84 #region 9-residue repeats (G-G-X-G-[DN] -D-X-[LVIE]-X)\	
721-729	721-738 #region repeat #status atypical\	
730-747	739-747 #region repeat\	
748-756	757-765 #region repeat #status atypical\	
766-774	766-774 #region repeat\	
775-783	775-783 #region repeat\	
784-792	784-792 #region repeat\	
793-801	793-801 #region repeat\	
812-820	812-820 #region repeat\	
821-829	821-829 #region repeat #status atypical\	
830-838	830-838 #region repeat\	
839-847	839-847 #region repeat\	
580,686	580,686 #binding-site palmitate (lys) (covalent) #status Predicted	
SUMMARY #length 1022 #molecular-weight 110013 #checksum 8625	Query Match Best Local Similarity 46.28; Pred. No. 7.96e-295; Matches 376; Conservative 201; Mismatches 206; Indels 31; Gaps 26;	Score 2291; DB 1; Length 1022;
Db 39	KOAGQKLILYIPKDYQAST-GSSNLNDLYKAEEALGIEVHRSEKGNTTAKALEFGTTEKL 96	REFERENCE #cross-references GB:x16829; PID:g38645 #note the authors present evidence that the nucleotide sequence is correct in the vicinity of amino acid 922. A37205 differs after this residue as a result of a frameshift from one missing nucleotide
Qy 11	KTGARKLILYIPKDYQAST-GSSNLNDLYKAEEALGIEVHRSEKGNTTAKALEFGTTEKL 96	Kraig, E.; Dailey, T.; Kolodrubetz, D. Infect. Immun. (1990) 58: 920-929 Nucleotide sequence of the leukotoxin gene from Actinobacillus actinomycetemcomitans: homology to the alpha-hemolysin/leukotoxin gene family. MUID:90202154
Db 97	LGFSGERGIAFAPQDKLNKRNQRKLSKPSLAKAGVDAQQLVNNTIASATGTVDAFAEQGLGNALSN 156	REFERENCE #cross-references GB:x16829; PID:g38645 #note the authors present evidence that the nucleotide sequence is correct in the vicinity of amino acid 922. A37205 differs after this residue as a result of a frameshift from one missing nucleotide
Qy 71	IGLTERGVNSAQPQDKLQKT-RAGOALG-SASIVQANAKTVALQSLIGTQTA 70	Kolodrubetz, D.; Dailey, T.; Eberson, J.; Kraig, E. Infect. Immun. (1989) 57: 1465-1469 Cloning and expression of the leukotoxin gene from Actinobacillus actinomycetemcomitans. A60768
Db 157	MDLDSSLRRRNGEDYGSGLPKLNKRNQRKLSKPSLAKAGVDAQQLVNNTIASATGTVDAFAEQGLGNALSN 216	REFERENCE #cross-references GB:x16829; PID:g38645 #note the authors present evidence that the nucleotide sequence is correct in the vicinity of amino acid 922. A37205 differs after this residue as a result of a frameshift from one missing nucleotide
Qy 129	MDLDSSLRRRNGEDYGSGLPKLNKRNQRKLSKPSLAKAGVDAQQLVNNTIASATGTVDAFAEQGLGNALSN 216	Kolodrubetz, D.; Dailey, T.; Eberson, J.; Kraig, E. Infect. Immun. (1989) 57: 1465-1469 Cloning and expression of the leukotoxin gene from Actinobacillus actinomycetemcomitans. A60768
Db 217	R-LGLASKLNNLPDLISLAGPFDAVSGLISVVASFELNSNKDADAGTAAAGLEIISTKL 275	REFERENCE #cross-references GB:x16829; PID:g38645 #note the authors present evidence that the nucleotide sequence is correct in the vicinity of amino acid 922. A37205 differs after this residue as a result of a frameshift from one missing nucleotide
Qy 184	KGLGTIDKLNKRNQRKLSKPSLAKAGVDAQQLVNNTIASATGTVDAFAEQGLGNALSN 216	Kolodrubetz, D.; Dailey, T.; Eberson, J.; Kraig, E. Infect. Immun. (1989) 57: 1465-1469 Cloning and expression of the leukotoxin gene from Actinobacillus actinomycetemcomitans. A60768
Db 276	LGNIGNAIGVSYTIAQRAAQLSITRATGGTAAAGLQVVAATGTVDAFAEQGLGNALSN 335	REFERENCE #cross-references GB:x16829; PID:g38645 #note the authors present evidence that the nucleotide sequence is correct in the vicinity of amino acid 922. A37205 differs after this residue as a result of a frameshift from one missing nucleotide
Qy 244	VGNITKAVSSKYLIAQRAAQLSITRATGGTAAAGLQVVAATGTVDAFAEQGLGNALSN 303	Kolodrubetz, D.; Dailey, T.; Eberson, J.; Kraig, E. Infect. Immun. (1989) 57: 1465-1469 Cloning and expression of the leukotoxin gene from Actinobacillus actinomycetemcomitans. A60768
Db 336	SERFKFGYEGDSLLASFYRETGALEAALTINTSVLSAASAGVGAATGSLVGAPVAALV 395	REFERENCE #cross-references GB:x16829; PID:g38645 #note the authors present evidence that the nucleotide sequence is correct in the vicinity of amino acid 922. A37205 differs after this residue as a result of a frameshift from one missing nucleotide
Qy 304	AERFKLGYGDNLIAEYQRTGTIDASVYPAINTALAAAGGYAAAASVIASPIALV 363	Kolodrubetz, D.; Dailey, T.; Eberson, J.; Kraig, E. Infect. Immun. (1989) 57: 1465-1469 Cloning and expression of the leukotoxin gene from Actinobacillus actinomycetemcomitans. A60768
Db 396	SAITGLISGLDASKOAIIFERVATKLANKTDEWEKK-HGKQNYFENGYDARHSAPLEDPE 454	REFERENCE #cross-references GB:x16829; PID:g38645 #note the authors present evidence that the nucleotide sequence is correct in the vicinity of amino acid 922. A37205 differs after this residue as a result of a frameshift from one missing nucleotide
Qy 364	SGITGVSTILQYSQAMFHVANKHNVKEWKKHGNQYFNGYDARYLNQDNMK 423	Kolodrubetz, D.; Dailey, T.; Eberson, J.; Kraig, E. Infect. Immun. (1989) 57: 1465-1469 Cloning and expression of the leukotoxin gene from Actinobacillus actinomycetemcomitans. A60768
Db 455	LLSQINKEYVERVVAITQQRWDYNGIELAGITRKSDTKSKAYVDFEEGKULEKEP 514	REFERENCE #cross-references GB:x16829; PID:g38645 #note the authors present evidence that the nucleotide sequence is correct in the vicinity of amino acid 922. A37205 differs after this residue as a result of a frameshift from one missing nucleotide

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           'VGTKRQFHLSPLDPDLRKIVSQVALCLLVLROCVLHKSPVQOMILVLFQQPV
           'VLVH', '#cross-references GB:M27933
REFERENCE A32216
#authors Lally, E.T.; Kieba, I.R.; Demuth, D.R.; Rosenblom, J. ;
          Golub, E.E.; Taichman, N.S.; Gibbons, C.W.
#journal Biochem. Biophys. Res. Commun. (1989) 159:256-262
#title Identification and expression of the Actinobacillus
          actinomyetomitans leukotoxin gene.
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          nucleic acid sequence not shown; not compared with
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##residues 430-438, 'S', '440-476, 'R', '478-506, 'RVRVS', '511,
           'QSAINSLNND', '523-541, 'I', '543, 'PQV', 'RKNG', '556, 'A',
           '558-589, 'MIFY', '594-689, 'ST', '693-723, 'N', '725-754
           ##label LA2
           ##note thus preliminary sequence has been revised in reference
           A34345
REFERENCE PHO266
#authors Ohta, H.; Miyagi, A.; Kato, K.; Fukui, K.
#submission submitted to JPJID, July 1995
#description Modulation of leukotoxin production by growth rate and
          bicarbonate in a toxin production-variable strain of
          Actinobacillus actinomyetomitans.
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##residues 2-6, 'L', '8-26 ##label OH2
COMMENT This organism is implicated in juvenile periodontitis.
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FUNCTION lyses human polymorphonuclear lymphocytes and monocytes
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KEYWORDS cytolysis; hemolysis; lipoprotein; periplasmic space; tandem
repeat
FEATURE
  245-790 "#domain hemolysin A homology # label HLYA \
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Best Local Similarity 46.1%; Pred. No. 7; 59e-283;
Matches 371; Conservative 189; Mismatches 210; Indels 34; Gaps 25;
Db 44 KTG-KKLTLVTPKNY---KGNGLTALIKAAOKLGLIEVYHEKGDKGPALTNGUUTNGKKL 98
Qy 11 KTGAKKILIPQNYDQTEQNGQDLYVAEEGLIEQREERNIAATQTSIGTIQPA 70
Db 99 LGTERGLTLPAPELDKWIQGNKHLNSVSGSTGNLTKAIDKVQSVLGTQOAFINTAFSGM 158

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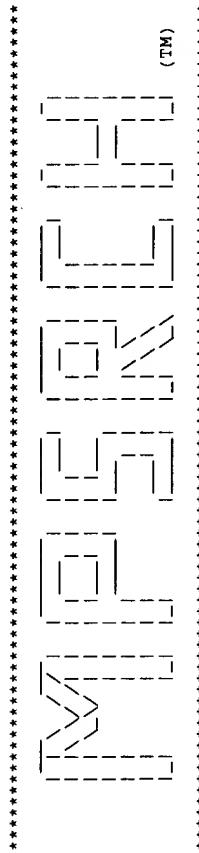
Db 884 DTTIDLAKVVSQSL-VD-AN-G-VLK-HSTKLDVIGGGDDVVYLANASRIHYDGGAGTNTV 938  
 Qy 550 SSTEFLTNVQRGILDNAGNTTKTKEIARKLGEDDDNVFVGSGSTEIDGEGDRV 609  
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 Qy 610 HYSR-GNYGALTIDATKETEQQSYTVNRFETGKALHEVTSHTALVGNREKIEYRHSN 668  
 Qy 995 LARVQGYVEVDTLEHQHHTGGAGNDTSITGAHDNFLLAGGSDDRLDGAGNTLVGEG 1054  
 Db 669 NQHHAGYXYTKDTLKAVEEITGSHNDIFKGSKRNDAFGDGTIDNGDNRLFGKG 728  
 Qy 1055 QNTVIGGAGDDVFLQDLGWSNLQDGGAGVDTYKVNHPSEERLERMGDGTHADL 1110  
 Db 729 DDILDGNGDD-FIDG-GKGNLHGGKG-DDI-F-VHRKGDN-DEITDSGNDKL 779  
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 ORGANISM #formal\_name Bordetella bronchiseptica  
 DATE 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change  
 23-May-1997  
 ACCESSIONS S51672  
 REFERENCES Betso, F.; Sismeiro, O.; Danchin, A.; Guiso, N.  
 #authors submitted to the EMBL Data Library, September 1994  
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 bronchiseptica.  
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 Db 588 ALAAARGTYSGLOVAGASAAGALAALSPMEIYGLVQOSHYADOLDKLAQESSAYG 647  
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Qy 550 SSTEDLTNVQRGILDNAGNTTKTKEIARKLGEDDDNVFVGSGSTEIDGEGDRV 609  
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 Qy 610 HYSR-GNYGALTIDATKETEQQSYTVNRFETGKALHEVTSHTALVGNREKIEYRHSN 668  
 Db 994 LARVQGYVEVDTLEHQHHTGGAGNDTSITGAHDNFLLAGGSDDRLDGAGNTLVGEG 1053  
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 ORGANISM #formal\_name Neisseria meningitidis  
 DATE 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change  
 09-Sep-1997  
 ACCESSIONS S35027  
 REFERENCES S35026  
 #authors Thompson, S.A.; Wang, L.L.; Sparling, P.F.  
 Mol. Microbiol. (1993) 9:85-95  
 #journal Cloning and nucleotide sequence of frpC, a second gene from  
 Neisseria meningitidis encoding a protein similar to RTX  
 #title  
 #cross-references GB:L06299; NID:9293961; PID:9293963  
 GENETICS frpC  
 #gene frpC  
 SUMMARY #length 1829 #molecular\_weight 197622 #checksum 8960  
 Query Match Score 4.6%; Score 286; DB 2;  
 Best Local Similarity 31.8%; Pred. No. 7.59e-18;  
 Matches 70; Conservative 60; Mismatches 71; Indels 19; Gaps 18;  
 Db 952 AKDDSGQVYQSYFQNQDGSAYRIDEHFDNGKVL DVATV KELYQSTDSDRLYAQ 1009  
 Qy 612 SRGNYGALTIDATKETE-QGSYTVNRE-VEIGKALHEVTSHTALVGNREKIE-YR-H 666  
 #molecule-type DNA  
 #residues 1-1829 #label THO  
 #cross-references GB:L06299; NID:9293961; PID:9293963  
 GENETICS frpC  
 #gene frpC  
 SUMMARY #length 1829 #molecular\_weight 197622 #checksum 8960  
 Query Match Score 4.6%; Score 286; DB 2;  
 Best Local Similarity 31.8%; Pred. No. 7.59e-18;  
 Matches 70; Conservative 60; Mismatches 71; Indels 19; Gaps 18;  
 Db 952 AKDDSGQVYQSYFQNQDGSAYRIDEHFDNGKVL DVATV KELYQSTDSDRLYAQ 1009  
 Qy 612 SRGNYGALTIDATKETE-QGSYTVNRE-VEIGKALHEVTSHTALVGNREKIE-YR-H 666  
 #molecule-type DNA  
 #residues 1-1829 #label THO  
 #cross-references GB:L06299; NID:9293961; PID:9293963  
 GENETICS frpC  
 #gene frpC  
 SUMMARY #length 1829 #molecular\_weight 197622 #checksum 8960  
 Query Match Score 4.6%; Score 286; DB 2;  
 Best Local Similarity 31.8%; Pred. No. 7.59e-18;  
 Matches 70; Conservative 60; Mismatches 71; Indels 19; Gaps 18;  
 Db 1010 SGNTLNGGL-GDDYLKGADGDLLNGDAGNDIYSGNG-NDTLLNGEGNDALYGYNGNDA 1067  
 Qy 667 SNNQHAGYTYRDTL KA-VEETI-G-TSHNDIFKGSKENDAFNGGDVTDIDGNQNDR 722  
 Db 1068 LNCGEENDHNLNGEDGNDTLIGGAGNDYLEGGSQSDTYYVFGKGFQDTVNYDYATGRKD 1127  
 Qy 723 LFGGKGDIDLGNGDDEIDGSKGNDLHGGDDLFVHRKGDGNDII-T-SDG-NDK 778  
 Db 1128 IRFTDGITADMLJTFREGNHLLIKADGSQVTQSYFON 1167  
 Qy 779 LSFSDSNIKRD-LTFEKVHNLYI-TNSKKEKVTIONWFR 816  
 Search completed: Wed Dec 9 19:23:12 1998  
 Job time : 176 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit.

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**MPSrch\_PP** protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:23:29 1998; MasPar time 25.63 Seconds

980.165 Million cell updates/sec

Tabular output not generated.

Title: >US-08-455-970-12

Description: (1-936) from US8455970.pep

Perfect Score: 6217

Sequence: 1 MATVIDLSPFPKTKRKKIIL.....LSSSOFARGSOHNSYGLRPG 936

Scoring table: PAM 150

Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0<sup>3</sup> summaries

Database: swiss-prot35

1:swissprot

Statistics: Mean 57.021; Variance 139.964; scale 0.407

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description	Pred. No.
1	6049	97.3	953	1 HIA1_PASHA LEUKOTOXIN FROM SEROTY	0.00e+00
2	574.3	92.4	953	1 HIA2_PASHA LEUKOTOXIN FROM SEROTY	0.00e+00
3	5560	89.4	953	1 HIA3_PASHA LEUKOTOXIN FROM SEROTY	0.00e+00
4	5510	88.6	955	1 HIAA_PASHA LEUKOTOXIN FROM SEROTY	0.00e+00
5	5020	80.7	947	1 HIIYA_PASSP LEUKOTOXIN.	0.00e+00
6	4254	68.4	956	1 RP2A_ACTPL RTX-II TOXIN DETERMINA	0.00e+00
7	4205	67.6	956	1 HIIYA_ACTSU HEMOLYSIN (CYTOLYSIN I	0.00e+00
8	2616	42.1	1052	1 RP32_ACTPL RTX-III TOXIN DETERMIN	0.00e+00
9	2566	41.3	1049	1 RP31_ACTPL RTX-III TOXIN DETERMIN	0.00e+00
10	2398	38.6	1023	1 HIIYA_ECOLI HEMOLYSIN, CHROMOSOMAL	0.00e+00
11	2384	38.3	1024	1 HIIYA_ECOLI HEMOLYSIN, PLASMID.	0.00e+00
12	2244	36.1	1023	1 RP12_ACTPL RTX-I TOXIN DETERMINAN	0.00e+00
13	2236	36.0	1023	1 RP11_ACTPL RTX-I TOXIN DETERMINAN	0.00e+00
14	2167	34.9	1050	1 HIIYA_ACTAC LEUKOTOXIN.	0.00e+00
15	896	14.4	1706	1 CYAA_BORPE CALMODULIN-SENSITIVE A	9.23e-119
16	887	14.3	1705	1 CYAA_BORPB CALMODULIN-SENSITIVE A	2.89e-117
17	286	4.6	1829	1 FRPC_NEIME IRON-REGULATED PROTEIN	8.54e-22
18	265	4.3	1115	1 FRPA_NEIME IRON-REGULATED PROTEIN	8.30e-19
19	202	3.2	491	1 ZAPA_PROMI EXTRACELLULAR METalloP	3.02e-19
20	187	3.0	476	1 LIPB_PSEFL LIPIASE PRECURSOR (EC 3	2.52e-08
21	173	2.8	284	1 NODO_PHILY NODULATION PROTEIN O.	1.38e-06
22	165	2.7	475	1 PRIG_ERWCH SECRETED PROTEASE G PR	1.29e-05
23	166	2.7	1 PRTC_ERWCH SECRETED PROTEASE C PR	9.75e-06	

24	170	2.7	481	1 PRTB_ERWCH SECRETED PROTEASE B PR	3.21e-06
25	164	2.6	472	1 PRTA_ERWCH SECRETED PROTEASE A PR	1.69e-05
26	162	2.6	478	1 PRTX_ERWCH SECRETED PROTEASE C PR	2.93e-05
27	159	2.6	3591	1 FHAB_BORBR FILAMENTOUS HEMAGGLUTI	6.02e-05
28	152	2.4	449	1 LIPA_PSEFL LIPIASE PRECURSOR (EC 3	4.31e-04
29	150	2.4	479	1 APRA_PSEAE ALKALINE METALLOPROTEI	7.30e-04
30	147	2.4	487	1 PRZN_SEMEA SERRALYSIN PRECURSOR (	1.60e-03
31	137	2.2	1574	1 MYS2_YEAST MYOSIN-2 ISOFORM	2.04e-02
32	133	2.1	486	1 PRZN_SERSP SERALYSIN PRECURSOR (	5.50e-02
33	133	2.1	550	1 KUCR_RAT KUPFER CELL RECEPTOR.	5.50e-02
34	132	2.1	749	1 MAD1_YEAST SPINDLE ASSEMBLY CHECK	7.02e-02
35	133	2.1	1959	1 MYSN_CHICK MYOSIN HEAVY CHAIN, NO	5.50e-02
36	133	2.1	2035	1 HFCL_HUMAN HOST CELL FACTOR C1 (H	5.50e-02
37	131	2.1	2249	1 190K_RICRI 190 KD ANTIGEN PRECURS	8.95e-02
38	122	2.0	390	1 FLRA_BORBR FLAGELLIN.	7.56e-01
39	122	2.0	682	1 PILJ_PSEAE PILJ PROTEIN.	7.56e-01
40	123	2.0	1025	1 SLAP CAUC S-LAYER PROTEIN (PARAC	5.99e-01
41	124	2.0	2541	1 TALL_MOUSE_TAIL TAIL MOUSE TAIL.	4.75e-01
42	121	1.9	344	1 Y09A_MYCTU HYPOTHETICAL 35.1 KD P	9.51e-01
43	121	1.9	409	1 Y291_METJA PROBABLE SIGNAL RECOGN	9.51e-01
44	121	1.9	754	1 KATC_ARIIA KINESIN-LIKE PROTEIN C	9.51e-01
45	121	1.9	2491	1 TALA_DICDI FILOPODIN (TALIN HOMOL	9.51e-01

### ALIGNMENTS

RESULT	1	STANDARD;
ID	HIA1_PASHA	PRT; 953 AA.
AC	P16535;	
DT	01-AUG-1990 (REL. 15, CREATED)	
DT	01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)	
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)	
DE	LEUKOTOXIN FROM SEROTYPE A1.	
GN	LTA.	
OS	PASTEURELLA HAEMOLYTICA.	
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; PASTEURELLACEAE.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=PH101 / SEROTYPE A1;	
RX	MEDLINE: 87306837	
RA	LO R.Y.C., STRATHDEE C.A., SHEWEN P.E.;	
RL	INFECT. IMMUN. 55:1987-1996(1987).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=PH101 / SEROTYPE A1;	
RX	MEDLINE: 89210283	
RA	HIGHLANDER S., CHIDAMBARAM M., ENGLER M.J., WEINSTOCK G.M.;	
RN	DNA 8:15-28(1989).	
[3]		
RP	SEQUENCE OF 894-953 FROM N.A.	
RC	STRAIN=PH101 / SEROTYPE A1;	
RX	MEDLINE: 9036888	
RA	HIGHLANDER S.-K., ENGLER M.J., WEINSTOCK G.M.;	
RL	RIB. BACTERIOL. 172:2343-2350(1990).	
CC	-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.	
CC	-!- SUBCELLULAR LOCATION: SECRETED.	
CC	-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.	
CC	-!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN POLE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).	
CC	-!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE STRUCTURAL TOXIN).	
CC	-!- EMBL: M20730; G150494; -.	
DR	EMBL: M24197; G150513; -.	
DR	PIR: S29516; S29516.	
DR	HSSE; P02392; ICIF.	
DR	PROSITE: PS00330; HEMOLYSIN_CALCIUM; 4.	
KW	KW TRANSMEMBRANE.	

FT	TRANSHEM	229	249	POTENTIAL.
FT	TRANSHEM	297	318	POTENTIAL.
FT	TRANSHEM	366	390	POTENTIAL.
FT	DOMAIN	734	784	6 X REPEATS, GLY-RICH ( BY SIMILARITY ).
FT	REPEAT	734	739	1.
FT	REPEAT	743	748	2.
FT	REPEAT	752	757	3.
FT	REPEAT	761	766	4.
FT	REPEAT	770	775	5.
FT	REPEAT	779	784	6.
FT	CONFLICT	409	414	FEHVN V -> LSTLQI ( IN REF. 2 ).
FT	CONFLICT	742	747	D -> Y ( IN REF. 2 ).
SQ	SEQUENCE	953 AA:	101996 MW:	4 0FB25EB CRC32;
Query	Match	953 AA:	Score 6049; DB 1;	Length 953;
Best	Local Similarity	99.8%	Pred. No. 0..0e+00;	
Matches	Conservative	2;	Mismatches 0;	Indels 0;
Db	38	KTGARKKILLYPQNQYDTEQNGLQLDLVKAEEGIEYQEREERNIATAQTSLGTTQTA	97	
Qy	11	KTGARKKILLYPQNQYDTEQNGLQLDLVKAEEGIEYQEREERNIATAQTSLGTTQTA	70	
Db	98	IGLTERGIVLSPQIDKLQLDKTQAGLSAESTYQNANKAKTVLGSQISILGSVLAGMD	157	
Qy	71	IGLTERGIVLSPQIDKLQLDKTQAGLSAESTYQNANKAKTVLGSQISILGSVLAGMD	130	
Db	158	LDEALQNSNOHALAKAGLELTNSLJENIANSVKTLDGEQISQFGSKLQNIGLGTG	217	
Qy	131	LDEALQNSNOHALAKAGLELTNSLJENIANSVKTLDGEQISQFGSKLQNIGLGTG	190	
Db	218	DLKLNTGGLDKAGLGLDVISGLSGATAAVLADKNASTARRYKAGFELANQVGNITRA	277	
Qy	191	DLKLNTGGLDKAGLGLDVISGLSGATAAVLADKNASTARRYKAGFELANQVGNITRA	250	
Db	278	VSSYLLAQRYAAGLSSGTGPVAAILASTVSLAISPLAFAAGTADKENHAKSLESYAEFRKKL	337	
Qy	251	VSSYLLAQRYAAGLSSGTGPVAAILASTVSLAISPLAFAAGTADKENHAKSLESYAEFRKKL	310	
Db	338	GYGDNLALAYQORGTTIDASVTAINTALAIAAGGVSAAAGSYTASPIALLVSGITGYI	397	
Qy	311	GYGDNLALAYQORGTTIDASVTAINTALAIAAGGVSAAAGSYTASPIALLVSGITGYI	370	
Db	398	STLQYSQAMFEHYANKIHKNIWEKRNHHGKNYFENGYDARYLNLQDNMKFLNNLRK	457	
Qy	371	STLQYSQAMFEHYANKIHKNIWEKRNHHGKNYFENGYDARYLNLQDNMKFLNNLRK	430	
Db	458	ELQAERYIAATQQODNINIGDLAGISRLGEKVLSKGAKVYDAFEEGKHAKDVKLYQDLSAN	517	
Qy	431	ELQAERYIAATQQODNINIGDLAGISRLGEKVLSKGAKVYDAFEEGKHAKDVKLYQDLSAN	490	
Db	518	GIIDVNSNSGAKTQHILFPRPLTGTHERVQTGKYKEYTKLNINRVDWSWLTDGAS	577	
Qy	491	GIIDVNSNSGAKTQHILFPRPLTGTHERVQTGKYKEYTKLNINRVDWSWLTDGAS	550	
Db	578	STFDLTNVORIGIELDAGNVTKTKETKIAKGEGDDNFVFSGGTEIDGGEGYDVRH	637	
Qy	551	STFDLTNVORIGIELDAGNVTKTKETKIAKGEGDDNFVFSGGTEIDGGEGYDVRH	610	
Db	638	YSRGNYGAALTDATKETEIQGSYTNRFVETGKALHEVTSTHTALVGNEEKIEYRHSSNQ	697	
Qy	611	YSRGNYGAALTDATKETEIQGSYTNRFVETGKALHEVTSTHTALVGNEEKIEYRHSSNQ	670	
Db	698	HHAGYYTKDTLKAVEEIIIGTSHNDLFPGSKFNDAPNGDCGVTDGNDGNDRLFGKGDD	757	
Qy	671	HHAGYYTKDTLKAVEEIIIGTSHNDLFPGSKFNDAPNGDCGVTDGNDGNDRLFGKGDD	730	
Db	758	ILDGGNGDDFLDGKGNDLJLHGKGDDDFVHRKGDDNIDTSDGNDKUSFSDSNLKDIT	817	
Qy	731	ILDGGNGDDFLDGKGNDLJLHGKGDDDFVHRKGDDNIDTSDGNDKUSFSDSNLKDIT	790	
Db	818	FEKVKHNVLVNTSKKEKVTIONWFREADFAKEYPKYATKDEKEEIJONGERITSKCV	877	
Qy	791	FEKVKHNVLVNTSKKEKVTIONWFREADFAKEYPKYATKDEKEEIJONGERITSKCV	850	

Db	878	DDLTKAGNGKKTQDELSKVVYDNYELLKHSKVNNTNSLDKLISSSVAFSTSSNDSRNVLYAPT	937
Qy	851	DDLIAGNGKKTQDELSKVVYDNYELLKHSKVNNTNSLDKLISSSVAFSTSSNDSRNVLYAPT	910
Db	938	SMLDQSLSLSSQFARA	953
Qy	911	SMLDQSLSLSSQFARGS	926
RESULT	2		
ID	HLAB_PASHA	STANDARD;	PRT; 953 AA.
AC	P55118;		
DT	01-OCT-1996	(REL. 34. CREATED)	
DT	01-OCT-1996	(REL. 34. LAST SEQUENCE UPDATE)	
DT	01-OCT-1996	(REL. 34. LAST ANNOTATION UPDATE)	
DE	LEUKOTOXIN FROM SEROTYPE All.		
GN	LKTA.		
OS	PASTURELLA HAEMOLYTICA		
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;		
OC	PASTURELLACEAE.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN SEROTYPE All;		
RX	MEDLINE; 94041617;		
RA	BURROWS L.L., OLAH-WINFIELD E., LO R.Y.C.;		
RL	INFECT. IMMUN. 61:5001-5007(1993).		
CC	-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD		
CC	CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY		
CC	DEFINED.		
CC	-!- SUBCELLULAR LOCATION: SECRETED.		
CC	-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING		
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC		
CC	ACTIVITY.		
CC	-!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE		
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).		
CC	-!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE		
CC	STRUCTURAL TOXIN).		
DR	EMLB;10215; G39799;		
DR	PROSTI; PS00330; HEMOLYSIN-CALCIUM; 4.		
KW	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;		
KW	TRANSMEMBRANE.		
FT	TRANSMEM	230	POTENTIAL.
FT	TRANSMEM	297	317
FT	TRANSMEM	381	POTENTIAL.
FT	DOMAIN	734	784
FT	REPEAT	734	739
FT	REPEAT	743	748
FT	REPEAT	752	757
FT	REPEAT	761	766
FT	REPEAT	770	775
FT	REPEAT	779	784
SQ	SEQUENCE	953 AA; 102206 MW;	321C9369 CRC32;
Query Match		92.4%	Score 5743; DB 1; Length 953;
Best Local Matches	85%	Similarity 93.4%; Pred. No. 0; 0.e+00;	Gaps
Matches	31;	Mismatches 23; Indels 0;	
38	KTGAKKIIYLTPKDYDTEKGNGLQDLVKAAEELGEVQEKEFGNDIAKAQTSLGTONV	97	
Qy	11	KTGAKKIIYLTPQTYDTEKGNGLQDLVKAAEELGEVQEERNNIATAQTSLGTONV	70
Db	98	LGLTERGIVLVSAPQDQLLQKTKVGAIAGSAENLTGFSAKTVLGSQTSLGSVLAGMD	157
Qy	71	TGLTERGIVLVSAPQDQLLQKTKAGGALGSAESTVQNANKAKTVLGSQTSLGSVLAGMD	130
Db	158	LDEAQKNSNEFLTAKAGLETLNSLIENTANSVKTIDAFGDOIQNLGSKLQNYKGSSLG	217
Qy	131	LDEAQKNSNOHALAKAGLETLNSLIENTANSVKTIDFEFGEIQSQFSSKLQNIGLGLG	190
Db	218	DKLKGISGFDKTSGLDVSSGLSGATAALVADKNASTSRYGAEGFLANQVGNITKA	277
Qy	191	DKLNKGGLDIAGLGIDDVSSGLSGATAALVADKNASTSRYGAEGFLANQVGNITKA	250

Db	278	VSSYLAQRYAAGLSSSTGPVAAIYSTVSIAISPLAFAGTADKFHNHAKSLESTAERFKKL	337	CC -!- ACTIVITY: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN POLE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).
Qy	251	VSSYLAQRYAAGLSSSTGPVAAIYSTVSIAISPLAFAGTADKFHNHAKSLESTAERFKKL	310	CC -!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE STRUCTURAL TOXIN).
Db	338	GYGDNLNLLAEYQRGTGTDRTSYTAINTALAAIAGGVSAAAGRGSYTASPIALYSGITGYI	397	CC DR EMBL: U01216; G39795; PROSITE: PS00330; KW HEMOLYSIS; TOXIN; CYTOLYSIS; REPEAT; CALCIUM;
Qy	311	GYGDNLNLLAEYQRGTGTDASVTAINTALAAIAGGVSAAAGRGSYTASPIALYSGITGYI	370	KW TRANSMEMBRANE
Db	398	STILOQSKQMFHEVANKTHNKTYWEKNNHGKNFENGDARYTANLQDNMKELLINK	457	KW POTENTIAL.
Qy	371	STILOQSKQMFHEVANKTHNKTYWEKNNHGKNFENGDARYTANLQDNMKELLINK	430	KW POTENTIAL.
Db	458	ELQAERVIATIQOQWDNNIGDLAGISRLGEKVLSGKAYDAFEEGSKHAKDLYQOLDSAN	517	DR DOMAIN 6 X REPEATS, GLY-RICH.
Qy	431	ELQAERVIATIQOQWDNNIGDLAGISRLGEKVLSGKAYDAFEEGSKHAKDLYQOLDSAN	490	FT REPEAT 1.
Db	518	GIDVNSNSGAKTQDILFRPPLTPGTDDERVOTGKYEYIKTLNINRVDWKYTDTGARS	577	FT REPEAT 743 739 2.
Qy	491	GIDVNSNSGAKTQDILFRPPLTPGTDDERVOTGKYEYIKTLNINRVDWKYTDTGARS	550	FT REPEAT 752 757 3.
Db	578	STFDTNVVORIGFIELDNAGNVTKTKEVKLAKLGAGDDNVFQSSTTEIDGGEGYDRYH	637	FT REPEAT 761 766 4.
Qy	551	STFDTNVVORIGFIELDNAGNVTKTKEVKLAKLGEGDDNVFQSSTTEIDGGEGYDRYH	610	FT REPEAT 770 775 5.
Db	638	YSGRNNGALTIDATEQSYTNRFETVGKALHEGTSTHTALVGNREEKIEYRHNSNQ	697	FT REPEAT 779 784 6.
Qy	611	YSGRNNGALTIDATEQSYTNRFETVGKALHEVTSTHTALVGNREEKIEYRHNSNQ	670	SQ SEQUENCE 953 AA: 101948 MW; EFED778E CRC32;
			Query Match 89.4%; Score 5560; DB 1; Length 953;	
			Best Local Similarity 89.2%; Pred. No. 0.00e+00;	
			Matches 817; Conservative 55; Mismatches 44; Indels 0; Gaps 0;	
Db	698	HHAGYTTKDTLKAVEEIIIGTSHNDLFKGSKFENDAFNGGCVDTIDGKDNDRLFGKGDD	757	38 KNGYKKITLIXIPDKYDGSQSGNQLDLYKAEEFLGIEVQEKEEGNDIATAQTSIGTON 97
Qy	671	HHAGYTTKDTLKAVEEIIIGTSHNDLFKGSKFENDAFNGGCVDTIDGKDNDRLFGKGDD	730	Qy 11 KTGARKKIIYIIPQNYDQEONGNLQDLVKAEEFLGIEVQEERENNIAATQTSIGTON 70
Db	758	IIDGGNGDDFTDGKGNDLHKGKDDIFVHRQGDNTIDDSGNDKLSFSDSNLKDLT	817	Db 98 IGLTERGIYLSAPOQLDKLQKKNVQALQSESSETAQNFSSQAKTVLSGVQISLGSVLAGMD 157
Qy	731	IIDGGNGDDFTDGKGNDLHKGKDDIFVHRKGDNDLITDSGNDKLSFSDSNLKDLT	790	Qy 71 IGLTERGIYLSAPOQLDKLQKTRQALQGAESVQANAKTVLSGQISLGSVLAGMD 130
Db	818	FEKVHNHLVITNSRKEVTKTIDQWREADFAKEVRYKATKDEKEEIGONGERITSKOV	877	Db 158 LDEALQNESDQTLIKAQGLELTSLENITANSYOTLDASFSEQIISQFGSXLQNYRGLGALG 217
Qy	791	FEKVHNHLVITNSRKEVTKTIDQWREADFAKEVRYKATKDEKEEIGONGERITSKOV	850	Qy 131 LDEALQNSNQHNLAKAGLELTSLENITANSYTLDEGEQIISQFGSXLQNTKGLGTLG 190
Db	878	DDLIAKGNGKTTQDELSKVYDNEYLLKHSKNTNSLDKLISSASAFTSSNDSRNVLYAPT	937	Db 218 DKLKNIGGDLKDGAGLHVYSGLISGATATAVLADKDASTAKTGAGFELANQVGNNTKA 277
Qy	851	DDLIAKGNGKTTQDELSKVYDNEYLLKHSKNTNSLDKLISSASAFTSSNDSRNVLYAPT	910	Qy 191 DKLKNIGGDLKDGAGLHVYSGLISGATATAVLADKNASTAKVGAGFELANQVGNNTKA 250
Db	938	SMDDQSLSSLOFARA 953		Db 278 VSSYTLAQRYAARLSSTGVAALLASTYFLAISPLSFQIADFKRSLENYAERFKKL 337
Qy	911	SMDDQSLSSLOFARG 926		Qy 251 VSSYTLAQRYAAGLSSTGVAALLASTYFLAISPLAFAGTADKENHAKSLES/AFERFKL 310
Db	998	RESULT 3 ID HLA3_PASHA STANDARD; PRT: 953 AA.		Db 338 GYEGLSLLAEYQHQTGTIDASVTAINTALAAIAGGSAAAGSVASPAFLALYSGITGYI 397
AC	01-OCT-1996	(REL. 34, CREATED)		Qy 311 GYDGNLLELEYQRTGTIDASVTAINTALAAIAGGSAAAGSVASPAFLALYSGITGYI 370
DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)		Db 398 STILOYSKAMFEHVANKTHNKTYWEKNNHGKNFENGDARYLANILODNMKELLINK 457
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)		Qy 371 STILOYSKAMFEHVANKTHNKTYWEKNNHGKNFENGDARYLANILODNMKELLINK 430
DE	LEUKOTOXIN FROM SEROTYPE T3.		Db 458 ELQERVIAITQOQWDNSNQDLAGISRLGKSLRUEKLVGKAYDAFEQGQHKLADKLVQLDASK 517	
GN	LKTA.		Qy 431 ELQERVIAITQOQWDNSNQDLAGISRLGKSLRUEKLVGKAYDAFEQGQHKLADKLVQLDASK 490	
OS	PASTURELLA HAEMOLYTICA.		Db 518 GIDVSNTGAKTOHILFPLTPGTTERERVOTGKYEYIKLNINRVDWSQIKDGAAS 577	
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; PASTEURILLACEAE.		Qy 491 GIIDVNSNSGAKTQDILFRPPLTPGTTERERVOTGKYEYIKLNINRVDWSKTDGAAS 550	
RN	[1]		Db 578 STEFDLTNVVORIGFIELDNAGNTVKTETKIVATLGDDDNFVGSGTITDGGEGYDRYH 637	
RP	SEQUENCE FROM N.A.		Qy 551 STEFDLTNVVORIGFIELDNAGNTVKTETKIVATLGDDDNFVGSGTITDGGEGYDRYH 610	
RX	STRAIN=SEROTYPE T3;		Db 638 YSRGNYGALTIDATEKPEGSQSYTNRFYFSKALHEVTSHTALVGNREKIEYRHNSNQ 697	
RA	MEDLINE; 94041617.		Qy 611 YSRGNYGALTIDATEKPEGSQSYTNRFYFSKALHEVTSHTALVGNREKIEYRHNSNQ 670	
RL	RAWS, L.L., LO R.Y., OLAH-WINFIELD E.; INFECT. IMMUN. 61:5001-5007 (1993).		Db 698 HHAGYTYKDTLKAVEEIIIGTSHNDLFKGSKFENDAFNGGCVDTIDGNDNDRFLFGKGEDD 757	
CC	-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.		Qy 671 HHAGYTYKDTLKAVEEIIIGTSHNDLFKGSKFENDAFNGGCVDTIDGNDNDRFLFGKGEDD 730	
CC	-!- SUBCELLULAR LOCATION: SECRETED.			
CC	-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC			

Ddb	758	ILDGGNGDDFIDGGGNILLGGKGVDLFGHGGDNGDSITEEGNDKLFSDSNLRDLT	817
Qy	731	ILDGGNGDDFIDGGGNILLGGKGDDIFVHKGDDNITISDGNDKLFSDSNLRDLT	790
Ddb	818	FERVNHLLVITNTKQEVYTIONWREAFAKTIONYATRDKIEELIGQNGERITSKQV	877
Qy	791	FEVKHNIVITNSKKEVYTIONWREAFAKEPVNPKATKDENIEELIGQNGERITSKQV	850
Ddb	878	DDLIAKGNGKIAOSELEKVVDDNYQLLKYSRDASNSDLKLISASSAFTSSNDSRNLASPT	937
Qy	851	DDLIAKGNGKTIODELSKVVDNYELLKHSKVNNTSNDKLKLISVSASFSSNDSRNLAVAPT	910
Ddb	938	SMLDPSSIIQFARA	953
Qy	911	SMLDQSLSLQFARGS	926
RESULT			
ID	HLAA_PASHA	STANDARD;	PRT;
AC	P55117;		955 AA.
DT	01-OCT-1996 (REL. 34, CREATED)		
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)		
DE	LEUKOTOXIN FROM SEROTYPE T10.		
GN	PASTEURELLA HAEMOLYTICA		
COS	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;		
OC	PASTEURELLACEAE.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-SEROTYPE T10;		
RA	LAINSON A. F., MURRAY J., DAVIES R. C., DONACHIE W.;		
RL	MICROBIOLOGY 14:2499-2507(1996).		
CC	-!- FUNCTION: BACTERIAL TOXINS ARE EXOTOXINS THAT ATTACK BLOOD		
CC	CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY		
CC	DEFINED.		
CC	-!- SUBCELLULAR LOCATION: SECRETED.		
CC	-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING		
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC		
CC	ACTIVITY.		
CC	-!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE		
CC	INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).		
CC	-!- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE		
CC	STRUCTURAL TOXIN).		
EMBL	Z26247; G400425;		
DR	PROSITE: PS00330; HEMOLYSIN CALCTUM; 4;		
DR	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;		
KW	TRANSMEMBRANE.		
KW	TRANSMEM	299	POTENTIAL.
KW	TRANSMEM	361	POTENTIAL.
KW	TRANSMEM	383	POTENTIAL.
KW	DOMAIN	736	6 X REPEATS, GLY-RICH.
KW	REPEAT	736	1.
KW	REPEAT	745	2.
KW	REPEAT	754	3.
KW	REPEAT	763	4.
KW	REPEAT	772	5.
KW	REPEAT	781	6.
SE	SEQUENCE	955 AA:	102187 MW:
SE			AA440AOA CRC32;
Query Match			
Best Local Similarity	88.6%	Score 5510; DB 1;	Length 955;
Matches	810;	Pred. No. 0.0e+00;	
	Conservative	Mismatches 46;	Indels 0;
		Gaps 0	
Ddb	40	KNGAKILYLIPKDYKVDGSGNGNLQDLYKVAEELGEVQKEBGNDIKAQTSLGQTQNV	99
Qy	11	KTGAKILYLIPQNYQDTEQNGNLQDLYKVAEELGEVQKEERNIATAQTSLGQTQTA	70
Ddb	100	LGTERGIVLVSAPOLKLQKTKAGQQLGSASIVQNANKTVLQGSIQILGSVLAGMD	159
Qy	71	IGTERGIVLVSAPOLKLQKTKAGQQLGSASIVQNANKTVLQGSIQILGSVLAGMD	130
Ddb	160	LDEALONESDOLTLAKAGLELTNSLENIANSVOTLDAFSEOISOFGSKLONVKIGLGALG	219

CC	- IS NOT HEMOLYTIC.	Db	694 QHAGYYTDTLKSVEETIGTSRNDIFKSKFDDAFAFGDGVNIDGNAAGNDRLFGGKGF 753
CC	- 1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.	Qy	671 RHAGYYTDTLKAEEETIGTSHDIFRSKENDAFNGDGTIDGNGNDRLFGGKGF 730
CC	- 1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOXIN (BY SIMILARITY).	Db	754 IIDGGDGDFDIDGQGDDILHGKGKNDLICTYK-G-NDSISDGGNDRLSFADSNLKDLT 812
CC	- 1- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE STRUCTURAL TOXIN).	Qy	731 IIDGGNGDFDIDGKGKNDLITOSDGNDLSDPSNLKDLT 790
CC	EMBL: L12148; G457618; DR PROTEIN: PS00330; HEMOLYSIN_CALCIUM; 4; KW HEMOLYSINS_TOXIN; CYTOLYSIS_CYTOTOXIN; REPEAT; CALCIUM;	Db	813 FEKVNHMITAVYKEKVTIONWREADYAKVHYNTQADKEEETIGROGERITSRQI 872
KW TRANSMEMBRANE	FT TRANSEM 154 170 POTENTIAL. FT TRANSEM 312 333 POTENTIAL. FT TRANSEM 393 414 POTENTIAL. FT DOMAIN 625 780 7 X REPEATS, GLY-RICH.	Qy	791 FEVKVHNIVITNSKEKVTIONWREADYAKEPVNYKATKDKEEETIGQNERITSKQV 850
FT REPEAT 625 630 1; FT REPEAT 730 735 2; FT REPEAT 739 744 3; FT REPEAT 748 753 4; FT REPEAT 757 762 5; FT REPEAT 775 780 6; SQ SEQUENCE 947 AA: 101559 MR: 1D59473B CRC32: 6	Db	873 DELIEKGKGKIDOSELERIAEASSALKESVNSLAKVSSAGAFASNDNRVGCVPT 932	
RESULT 6 ID RT2A-ACTPL STANDARD; PRT; 956 AA.	Qy	851 DDLLAKRGKIKTDELSSVVDVNDYLRSKNTVNSDRSLSSVAFSTSNDSRNVLAAPT 910	
AC P15377; REL 14, CREATED) ID RT2A-ACTPL DT 01-APR-1990 (REL 14, LAST SEQUENCE UPDATE) DT 01-APR-1990 (REL 14, LAST SEQUENCE UPDATE)	Db	813 FEKVNHMITAVYKEKVTIONWREADYAKVHYNTQADKEEETIGROGERITSRQI 872	
RC STRAIN=SEROTYPE 5; RX DE RTX-II TOXIN DETERMINANT A (APX-IIA) (HEMOLYSIN IIA) (HLY-IIA) DE (COTOLYSIN IIA) (CLY-IIA). GN OS ACTINOBACILLUS PLEUROPNEUMONIAE (APPA OR APPA OR CYTCA) OC PROKARYOTA, GRACILICUTES, SCOTORBACTERIA, FACULTATIVELY ANAEROBIC RODS; OC PASTURELLACEAE.	Qy	791 FEVKVHNIVITNSKEKVTIONWREADYAKEPVNYKATKDKEEETIGQNERITSKQV 850	
RN SEQUENCE FROM N.A. RP STRAIN=SEROTYPE 5; RN DNA: 9016233; RA CHANG Y.-F.; YOUNG R., STRUCK D.K.; RL DNA 8: 635-64 (1989).	Db	94 LGFSGERVVLSAPOOLDKLQQYKISKAPESSENYVAKNQNLQNLGSQISLGSMAGMD 153	
Qy	71 IGLTERGIVLSSAPOOLDKLQQYKISKAPESSENYVAKNQNLQNLGSQISLGSMAGMD 130		
Db	154 LDETLKNGKSELDLAKAGLLETNLSTENANSVOTLDTPESEQIQLGKLNQYKGLGTLG 213		
Qy	131 LDEALQNSNSQHALAKAGLLETNLSTENANSVYTLDEFQEQISQFGSXLONIKGLGTLG 190		
Db	214 DKLKNFGESKAGLGLEVISGLSGLSGATAALYLDKNASTDYKAGFELANQVYGNITKA 273		
Qy	191 DKLKNGGIDKAGLGLDVSGLSGLSGATAALYLDKNASTDYKAGFELANQVYGNITKA 250		
Db	274 VSSYLAQRVAAGLSNTGPSALIASTVALAISPLAFAGTAKEFNNAKALESYAERFKL 333		
Qy	251 VSSYLAQRVAAGLSNTGPSALIASTVALAISPLAFAGTAKEFNNAKALESYAERFKL 310		
Db	334 GYEGRDSSLAEYORGSTGTIDASVTANTALAAISGGVSAAAAGSLVGAPELLVSGITGII 393		
Qy	311 GYDGNNLAAEYQRGTTGTDASVTANTALAAISGGVSAAAAGSVTASPLAVLGSITGVI 370		
Db	394 STILOYSKQAMFEHYANKIHDKIDWEKKHNGKMYFENGDSRYLADQDMRQLQNLNK 453		
Qy	371 STILOYSKQAMFEHYANKIHDKIDWEKKHNGKMYFENGDSRYLADQDMRQLQNLNK 430		
Db	454 ELQAERVIRITQQDNNIGNLAGISRLGEKVMSSGKAYDAFEGKLKADTFVQDSLAT 513		
Qy	431 ELQAERVIAITQQDNNIGNLAGISRLGEKVLQDSKAYDAFEGKHAKDQLVQDSLAT 490		
Db	514 GVINTSKSDNVKTQTHLFITPILJTPGVENRERIOTGKEYTKLNINRVDSWKTIDGATN 573		
Qy	491 GIDVDSNSGRAKTONHLFTRPLJPGTEERVOTGKEYTKLNINRVDSWKTIDGATN 550		
Db	574 SIEDLTNYVORIGFIELDHADNVTKTKEKTIANLGDNDVPIGSGETEVGGNGLDRYH 633		
Qy	551 SIEDLTNYVORIGFIELDHADNVTKTKEKTIANLGDNDVPIGSGETEVGGNGLDRYH 610		
Db	634 YSRGDYGAUJTDATNEVSQGSSYTKRFVETGKALHEVTQSVLVGSREEKIEYRHSNNT 693		
Qy	611 YSRGYGAUJTDATKETEQSYTVNRFVETGKALHEVTQSVLVGSREEKIEYRHSNNO 670		

FT	REPEAT	755	5.		RESULT	7	HYA_ACTSU	STANDARD;	PRT:	956 AA.
FT	REPEAT	764	6.		AC	Q00951;				
FT	REPEAT	773	7.		DT	01-APR-1993	(REL. 25, CREATED)			
FT	REPEAT	782	8.		DT	01-APR-1993	(REL. 25, LAST SEQUENCE UPDATE)			
SO	SEQUENCE	956 AA;	102531 MW;	6FBFBBFD CRC32;	DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)			
Query Match	Best Local Similarity	68.4%	Score 4254; DB 1; Length 956;		DE	HEMOLYSIN (CYTOLISIN II) (CLY-IIA) (HLY-IIA) (CYTC) (APPA).				
Matches	615; Conservative	67.1%	Pred. No 0.00e+00;		GN	APPB OR CLYIIA OR HLYIIA OR CYTC.				
Db	45 GARKKILYIPOGY- -DSCQGNGQDLYKAANDLGIEVWEEERSNLDTAKTSFDTTOKILG 102		155; Mismatches 139; Indels 8; Gaps 7;		OS	ACTINOBACILLUS SUIS				
Qy	1.3 GARKKILYIPOGYDQEKGNGQDLYKAADLGIEVQRENNNIAATQTSIGTQTAIG 72				OC	GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;				
Db	103 FTRGIVLFAPOLDNLKKRNPKIGNLTGSASSISQNIGKANTVIGQIQLSIVSGVNL 162				OC	PASTEURELLACEAE.				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				RN					
Db	163 NELLQNKDPNOQELAKAGLELTNVELNEYNIASSVOTVDAFABISKLGHSLNQVKGLGGLS 222				RP	SEQUENCE FROM N.A.				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				RC	STRAIN=3714;				
Db	132 DEFLQN NSNQHALAKAGLELTNSLIENNTVAKTMLVSKVTKLDFEISQFSKLQNKGLGTG 190				RX	MEDLINE: 92267623.				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				RA	BURROWS L., L., LO R.Y.;				
Db	223 NKLQNLPLDGKASLGLDUDTISGLLSGASAGNLADKEAESTEKKAAGYEFAANOQIIGNVTKA 282				CC	- I - FUNCTION: ONE OF THE VIRULENCE FACTORS OF A Suis. MIGHT BE A SECRETED CTIOTOXIN, POSSIBLY THE EXTRACELLULAR HEMOLYSIN.				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				CC	- I - SUBCELLULAR LOCATION: SECRETED.				
Db	191 DUKKNIGLGDKGAGLGLDVTISGLISGATAALVADKNASTAKVGAGFELAQVVGNTKA 250				CC	- I - DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				CC	- I - DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).				
Db	283 VSSYLLAQORVASSLSSTGPVALIATVAVSPLSPLNVAKEPQADLKYSSEFQKL 342				CC	- I - SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE STRUCTURAL TOXIN).				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				CC	CC				
Db	343 GWDGDRLLADEHREGTGTDASVTTINFALAAISGGVAASAGSLYQAPVALLVAGVTGLI 4 02				DR	EMBL: M90440; GI:141828;				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				DR	PROSITE: PS00330; HEMOLYSIN_CALCIUM; 1.				
Db	311 FGDDNLNLAEYQRTGTIDASVTTINFALAAISGGVAASAGSLYQAPVALLVAGVTGLI 402				KW	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				KW	TRANSMEMBRANE.				
Db	403 TTYLTSKQAMFEHVANKVHDIVERWEKK - HKKNYFEGQDSRHLADLODNEKFILNLNK 4 61				FT	TRANSMEM 238	254			
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				FT	TRANSMEM 302	320			
Qy	371 STLQYSKQAMFEHVANKVHDIVERWEKKHKNYFENGVDARYLANLQDNMKFLNLNK 4 30				FT	TRANSMEM 383	406			
Db	462 ELQAERVVAITQOQRDNOQIGDLAAISRTDKLSSGKAYDAFEEGHQSYDSVQLDNKN 521				FT	DOMAIN 719	799			
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				FT	REPEAT 719	724			
Db	431 ELQAERVVAITQOQRDNOQIGDLAAISRTDKLSSGKAYDAFEEGHQSYDSVQLDNKN 4 90				FT	REPEAT 728	733			
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				FT	REPEAT 737	742			
Db	522 GININISNTNR-KTQSVLERTPLTPGTGEBENREIQEGKNSYTKLHQRFQDSTWVTDGDS 580				FT	REPEAT 746	751			
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				FT	REPEAT 755	760			
Db	491 GIDDVSNSGKATQHILFERTPLTPGTPEHREHQVQTGKEYTKLNRDWSKHTDGAAS 550				FT	REPEAT 764	769			
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				FT	REPEAT 773	778			
Db	581 SYDFTNVYORVAYKGVDDNAGNTESKTKIILAGNDNYFVGSSNTVIDGGDHDRVH 640				FT	REPEAT 782	787			
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				FT	REPEAT 794	799	9.		
Db	551 STPDLTNVQRGIELDNAGNTKTKIKLGEEDDNVFGSGTEIDGEGGDRVH 610				SO	SEQUENCE 956 AA; 102453 MW; 85F73730 CRC32;				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Query Match	67.6%	Score 4205;	DB 1;	Length 956;	
Db	641 YSRGEYGAIVDATAETEKGSYSVKRYVGDSKSKALHETIAHTQVNGNREKELEYREDDR 700				Best Local Similarity	66.4%	Score 4025;	DB 1;		
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Matches	609;	Conservative 158;	Mismatches 142;	Gaps 8;	
Db	611 YSRGNYGALTIDATKETEQGSTVNREVEGTALHEVSTTHALVNRREEKTYRHNSNNQ 670				Db	45 GAKKLILYIPOGY - DSGCGNGIODYLKVAANDLGIEVWEEERSNLDTAISFTDTQKILG 102				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	13 GAKKLILYIPOQYDTEQNGLQDVKAAEELGIEVQEBERNNTATASLGLTQIATAG 72				
Db	701 FHGTGTYTDSLKSVEIIGSQNDIFGSKQFFDVPHQNGVDTIDGNDGDDHLEFGAGDD 760				Db	103 NELLQKDPNQELLAKEGLLTNEVGNASSSYTVDAEIQSRLGSHLQNYRGGLGGJS 222				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	132 DEALQVNLNQHAKAGLELTNSTVLTDECEISQFGLSNQNLQNGLGTG 190				
Db	671 HAGYITKDTIKAAYEETGTSNDIFGSKQFFDAFNGDGTIDTNDGNDLFGKGDD 730				Db	223 NKLQNLPDGLKASLGLDUSGGLSGASGLLAKASTEKKAAGVEFANQIQLGTVN 162				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	73 LTTERGTVLAPSQIDKLLQKT-KAGQALGSAESTVQNANAKTAKVLSQISLGSYLAGML 131				
Db	761 VDQGNGNFIYGGTGTGNDIISGGKNDTYYHKTGQDNDSTSISGGKDLSAFDVNLKDLT 820				Db	163 NELLQKDPNQELLAKEGLLTNEVGNASSSYTVDAEIQSRLGSHLQNYRGGLGGJS 222				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	132 DEALQVNLNQHAKAGLELTNSTVLTDECEISQFGLSNQNLQNGLGTG 190				
Db	731 ILLOGNGDDFIOGKGNGLLHGKGDDIFVHKRGKDGTIDTSDGNKLSFDSNJKDLT 790				Db	223 NKLQNLPDGLKASLGLDUSGGLSGASGLLAKASTEKKAAGVEFANQIQLGTVN 162				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	73 LTTERGTVLAPSQIDKLLQKT-KAGQALGSAESTVQNANAKTAKVLSQISLGSYLAGML 131				
Db	821 EKKYDSSLEIINQKGEKYRGINWLEDDLASTVANYKATNDKIEETIGKGERITSEQV 880				Db	163 NELLQKDPNQELLAKEGLLTNEVGNASSSYTVDAEIQSRLGSHLQNYRGGLGGJS 222				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	132 DEALQVNLNQHAKAGLELTNSTVLTDECEISQFGLSNQNLQNGLGTG 190				
Db	791 FERKVHNWITVSKKEKTVIQMWFREADFKEVNPYKATDKDKEEELGQNERITSKQV 850				Db	223 NKLQNLPDGLKASLGLDUSGGLSGASGLLAKASTEKKAAGVEFANQIQLGTVN 162				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	73 LTTERGTVLAPSQIDKLLQKT-KAGQALGSAESTVQNANAKTAKVLSQISLGSYLAGML 131				
Db	881 DLIKEGNNQISAEALSKVNDYNTSKDRQVNSLAKLISSEVGFTSSDFRNNGTYY 940				Db	163 NELLQKDPNQELLAKEGLLTNEVGNASSSYTVDAEIQSRLGSHLQNYRGGLGGJS 222				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	132 DEALQVNLNQHAKAGLELTNSTVLTDECEISQFGLSNQNLQNGLGTG 190				
Db	851 DDIJAKNGKTIODELSKVKDYELLIKHSKNTVNSLAKLISSEVGFTSSDFRNNGTYY 909				Db	223 NKLQNLPDGLKASLGLDUSGGLSGASGLLAKASTEKKAAGVEFANQIQLGTVN 162				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	73 LTTERGTVLAPSQIDKLLQKT-KAGQALGSAESTVQNANAKTAKVLSQISLGSYLAGML 131				
Db	941 PSSIDVSNNIQIARAA 956				Db	223 NKLQNLPDGLKASLGLDUSGGLSGASGLLAKASTEKKAAGVEFANQIQLGTVN 162				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Qy	73 LTTERGTVLAPSQIDKLLQKT-KAGQALGSAESTVQNANAKTAKVLSQISLGSYLAGML 131				
Db	910 TSMQDLSLSSLOFARG 926				Db	223 NKLQNLPDGLKASLGLDUSGGLSGASGLLAKASTEKKAAGVEFANQIQLGTVN 162				
Qy	: : : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :				Db	223 NKLQNLPDGLKASLGLDUSGGLSGASGLLAKASTEKKAAGVEFANQIQLGTVN 162				

311	GVDGDNLLAEGYRGTTGTIDASVTAINTALAAFTAGGYSAAGSVTASPIALVSGITGV	370
403	TITLEYSQAMPEHANKVHDRVWEKK - HNKYFEQGDYRSRHLADLQDNMKFLINLNK	461
371	STLQVSQAMPEHANKVHDRVWEKK - HNKYFEQGDYRSRHLADLQDNMKFLINLNK	430
462	ELQAEVERTAITQQWDNQIGDLAASRTDKISSKGKAYDAFEEGNTSPSPSIHDNDK	521
431	ELQAEVERTAITQQWDNQIGDLAISLGEKVLGRAYDVEEGHKIKAQLQYDSDA	490
522	GINISNTNR-KTQSVLFLRTPLPGENRERIQEAGNSYTKLHQFRDWSWTVTIVGDAS	580
491	GLIDVSNSGAKTQHILFRTPLPPTGEHEREVYOTCKYEYLTKLNNRVDWSWTKITGAAS	550
581	SSYDFTNVQRIAVKFDAGNITESDQTKLANLAGNDNFVGSSSTVTDGGDHDHRVH	640
551	SPFDLTVNVQRIGEELDNGNTYTRKETKATLGEDDDNVFGSGTEIIGEGDHRVH	610
641	YSRGEXYCALVIDATAETEKGGSYSKRYVGDSKALHETIATHOTNYGNREEKIEYREDDR	700
611	YSRGNYGAITDQATKETEQGSYTNVRVEGTGRALKHEVTSHTALYGNGREEKIEYRSNNQ	670
701	FHGTGTYTDSLSKEETIGSQNDIFKGSQFDDFHGGNGVDTIDGNDGDDHFLGAGDD	760
671	RHAGYYTKDTLKVAEELTGSTHNDIFGSKSKENDAFNGDGVDTIDGNDGNDRFLGSKGD	730
761	VTDGGNGNINFYGGTGTNDIISGGKDNDIYVHKTGNDGSDITDGGODKLAFLSDVNLRKDLT	820
731	ILDGGNDNEDDIFDGKGDRLLHKGKDDIFVARKGNDIITDSDGNDKLSFSNDNKRKDLT	790
821	EKKVQDSLEINOKGEGVRIGNWFLEDDLASTVANYKATNDRKIEELIGKGERITSEQV	880
791	FEKVKHNWVITQSKKEKTVQNSWREADFAKEPVYKPAKTDKIEELIGQNGERITSQKV	850
881	DKLKEGNQISAEALSKVWVNYNTSEDRQVNSNLAKLISSEVGFTSSSFERNNGTIV	940
851	DDLIAKNGKTKTQDELSKVVDNEYLLKHSKNVNTNSLDKLISSYSAFTSSNDSRNVLYA-P	909
941	PSSIDVS-NNIQLARA 956	
	:   :   :   :   :	
910	TSMDQSLSSQFARGC 926	
	:   :   :   :   :	
RESULT	8	
0	RH32_ACTPL	STANDARD;
0	PRT;	1052 AA.
0	PSS131;	
0	01-OCT-1996 (REL. 34, CREATED)	
0	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)	
0	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)	
0	RPX-III TOXIN DEPENDANT FROM SEROTYPE 8 (APX- IIIA) (CYTOLYSIN IIIA) (CLY- IIIA).	
0	ACTINOBACTERIUM PLEURONEUMONIAE (HAEMOPHILUS PLEURONEUMONIAE).	
0	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS.	
1	[1]	SEQUENCE FROM N.A.
1	SPRAINS-SEROTYPE 8;	
1	MEDLINE; 93162836;	
1	JANSSEN R., BRIAIRE J., KAMP E.M., GIELKENS A.L.J., SMITS M.A.;	
1	INFECT. IMMUN. 61:9417-954(1993).	
-1	FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT SHOWS A STRONG CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES AND NEUTROPHILS.	
-1	SUBCELLULAR LOCATION: SECRETED.	
-1	DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING	



Qy	364	SGTGVVSTIQLYSKQMFHVKANKTINKIVWEKNNGKNTFENGYDARYLNLQDNMK	4.23
Db	458	IISQYNKEYSVRSVLITQQHVDLIGELAGATRDTLSGRSYIDYYEGRKLEKKPD	5.17
Qy	424	FLLNLINEFLQAERVIATQQQMNNICLAGTSRIGEVYLSGRAYDVAEEGKHI - KAD	4.81
Db	518	EFOKQVDFPLKGNDLSDS-KSSST-LRKFTPLTPGEIRERRSGKYEITTELLVKY	5.75
Qy	482	KLV-QL-DSANGLIDVNSRSGKAKTOHLFRTPLTGPTEHRREVTKYEVYTKLNINRV	5.39
Db	576	DXWTKVQGDQKGSVYDMSNLQHASY----GN-NQXREIRISHLGODDKKFVLSAGSA	6.29
Qy	540	DSWKITDGA-SSTEDLTVNVQRIGIELDNAGNVTKIKETKLIAKLGESDDNYFGVSGTT	5.98
Db	630	NTYAGKHDVVYVYDKTDIGLYLTIDGTAKATEAGNVTTRVLGGDVKVLQEVVKKEQEVSGK	6.89
Qy	599	EIDGEGYDVRHVSRGNGALITDADETEQGYTVNRVETK-KALHVTSTHALVGN	6.57
Db	690	RTEKTOYRSYEETHINGKNLTEDNLYSVEELTGTTADKFFGSKFAIDFHGADGDHIE	7.49
Qy	658	REEKIEHRHNNNOHHAG-YYT-KDTLKAVEEIIITGHNDIEFKSKFNDAFGNGDQVTDID	7.15
Db	750	GNDGNDLQYDGDKNDTLSGGNGDQLLGGDGNDKLLIGAGANN-YLN-GSDGDD	8.00
Qy	716	GNDGNDLFGGRGDDILDGGNGDDEFIDGGKGNDLHGKGDDIFVHRKGDGND	7.68
RESULT	11		
ID	HILVA_ECOLI	STANDARD;	PRT; 1024 AA.
AC	PF08715;		
DT	01-JAN-1988	(REL. 06, CREATED)	
DT	01-JAN-1988	(REL. 06, LAST SEQUENCE UPDATE)	
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)	
DE	HEMOLYSIN, PLASMID.		
GN	HILVA.		
OS	ESCHERICHIA COLI.		
OG	PLASMID PHILY152.		
OC	PROKARYOTA; GRACILICUTUS; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIAE.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	HESS J., WELS W., VOGEL M., GOEBEL W.:		
RL	FEMS MICROBIOL. LETT. 34:1-11(1996).		
CC	- I - FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.		
CC	- I - SUBCELLULAR LOCATION: SECRETED.		
CC	- I - DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY.		
CC	- I - DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.		
CC	- I - DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY BY STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE OF THE URINARY TRACT.		
CC	- I - SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE STRUCTURAL TOXIN):		
DR	EMBL: M14107; G15068;		
DR	PROSITE: PS00330; HEMOLYSIN_CALCTUM; 4.		
KW	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN; REPEAT; CALCIUM;		
KW	TRANSMEMBRANE; PLASMID.		
FT	TRANSMEM 238	260	POTENTIAL.
FT	TRANSMEM 266	327	POTENTIAL.
FT	TRANSMEM 326	411	POTENTIAL.
FT	TRANSMEM 365	411	POTENTIAL.
FT	DOMAIN 724	870	16 X REPEATS, GLY-RICH.
FT	REPEAT 724	729	
FT	REPEAT 724	738	
FT	REPEAT 733	742	
FT	REPEAT 742	747	
FT	REPEAT 751	756	
FT	REPEAT 760	765	
FT	REPEAT 769	774	
FT	REPEAT 778	783	

DT	01-NOV-1997	(REF. 35, LAST ANNOTATION UPDATE)
DE	RTX-I TOXIN DETERMINANT FROM SEROTYPES 5/10	(APX-IA) (HEMOLYSIN IA)
DE	(HLY-IA) (CYTOLYSIN IA) (CLY-IA).	
GN	APXIA OR CLYIA OR HLYIA.	
OS	ACTINOBACILLUS PLEUROPNEUMONIAE (HAEMOPHILUS PLEUROPNEUMONIAE).	
OC	PROKARYOTAE, SCOTOBACTERIA, FACULTATIVELY ANAEROBIC RODS.	
OC	PASTEURELLAACE.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=13639 / SEROTYPE 10;	
RX	MEDLINE: 94276858.	
RA	NAGAI S.; YAGIHASHI T.; ISHIHAMA A.;	
RL	MICROB. PATHOG. 15: 485-495(1993).	
RN	[2]	
RC	STRAIN=K17 / SEROTYPE 5;	
RX	MEDLINE: 96401417.	
RA	CHIN N.; FREY J.; CHANG C.F.; CHANG Y.F.;	
RL	FEMS MICROBIOL. LETT. 143:1-6(1996).	
RN	[3]	
RP	SEQUENCE OF 886-1023 FROM N.A.	
RC	STRAIN=K17 / SEROTYPE 5;	
RX	MEDLINE: 93366425.	
RA	JANSEN R.; BRAIE J.; KAMP E.M.; GIELRENS A.L.J.; SMITS M.A.;	
RL	INFECT. IMMUN. 61:368-3695(1993).	
CC	- - FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPNEUMONIAE,	
CC	WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOXIC FOR	
CC	ALVEOLAR MACROPHAGES AND NEUTROPHILS.	
CC	- - SUBCELLULAR LOCATION: SECRETED.	
CC	- - DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING	
CC	CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC	
CC	ACTIVITY.	
CC	- - DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE	
CC	INVOLVED IN POSE FORMATION FOR THE CYTOTOXIN (BY SIMILARITY).	
CC	- - APXIA IS PARTIALLY DELETED IN SEROTYPES 2, 4, 6, 7, 8, 12, AND	
CC	TOTALLY DELETED IN SEROTYPE 3.	
CC	- - THE SEQUENCE SHOWN IS THAT OF SEROTYPE 10.	
CC	- - SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE	
CC	STRUCTURAL TOXIN).	
DR	EMBL: D16382; G497787; -.	
DR	EMBL: U04954; G1477457; -.	
DR	EMBL: X73116; G312151; -.	
DR	PROSITE: PS00330; HEMOLYSIN.CALCIUM; 2.	
KW	HEMOLYSIS; TOXIN; CYTOLYSIS; CYTOTOXIN;	
KW	TRANSMEMBRANE.	
FT	TRANSMEM 226	256
FT	TRANSMEM 297	326
FT	TRANSMEM 367	406
FT	DOMAIN 722	845
FT	REPEAT 722	727
FT	REPEAT 722	1.
FT	REPEAT 731	736
FT	REPEAT 740	2.
FT	REPEAT 749	745
FT	REPEAT 758	4.
FT	REPEAT 763	5.
FT	REPEAT 772	11.
FT	REPEAT 776	6.
FT	REPEAT 781	13.
FT	REPEAT 785	7.
FT	REPEAT 790	8.
FT	REPEAT 794	9.
FT	REPEAT 799	9.
FT	REPEAT 813	10.
FT	REPEAT 822	10.
FT	REPEAT 831	11.
FT	REPEAT 836	12.
FT	REPEAT 840	13.
FT	CONFFLICT 210	217
FT	CONFFLICT 581	AMPYLTIA -> GNALSNTR (IN REF. 2).
FT	CONFFLICT 687	E -> Q (IN REF. 2).
FT	CONFFLICT 688	TC -> R (IN REF. 2).
FT	CONFFLICT 1015	F -> L (IN REF. 2).
SO	SEQUENCE 110129	BD696433.CRC32.
DDB	4 3 RNAGNRLLILLPKDYK-G--QSSSLNDLVRITADELGIVDYEVOYDEKNATAITKQVFSTAEKL 99	
DQ	11 KTGARKKILYIFQNYQDTEQNGLQLVKAAEELGIVDYEVRERNNITQTSCTGTTQTA 70	
DDB	100 IGLTERGTIFTAPQLQDKLQYOKAGNLIGGAAENTGDNLKGAGGLTSLTFONFLGTALLS 159	
DQ	71 IGLTERCIVLSPASQDILQLQK-TKAQALGS-AESTVNANKAKTVLGSQISLGSVL 128	
DDB	160 MKIDELIKKQSGGNVSSSELAKASIELLNLQDVTIASLANNNVNTSQNTLGSVLNT 219	
DQ	129 MDLDEAL-QNNS-N-OHA-LAKAGLELTNSLIENTANSVKTLDLDFEQISQFGSKLQNI 183	
DDB	220 KHLNGVGKLNQLNPLDQNIGAGLDTVSGLSISAISAFILSNAADATRKAAGVELTTKV 279	
DQ	184 KGLGTQDCKLANYGGLDQAGLDTVSGLSAGATLVLADKNASTAKVYAGFELANV 243	
DDB	280 LGNVGKSIQSYTIAQRAAGLSTSAAAGLJASAYTIALISPLSLSIAIDAEKRANKIEY 339	
DQ	244 VGNITKAVSSYLQRAQVAGLSSTGPVAIIASLISLAFLAGIADEKFENHARSLEY 303	
DDB	340 SORFKKQYGDGSLLAARFHKEGAIDASLTISTVIAVSQGSIASATATLVSQGPAVSALV 399	
DQ	304 AERFKKQYGDGNLALAEYQRSTGTIDASVTAINTALAAIAGVSAAGGSVIASIALLV 363	
DDB	400 GAVTGIIQGLEAKSQAQMFEHVASKMDVIAWEKK-HGKNYFENCYDARHAAFLEDNPX 458	
DQ	364 SCITGVSTIOLYSKQMFHEANKHNKIVEWKENHGNYFENCYDARYLANQDNMK 423	
DDB	459 ILSQYKNEYVERSVLITQHQWDLTIGELAGVTRNGDKTLSGKSVDYEGKREKXD 518	
DQ	424 FFLNLNLKREQAVRIATQQMDNNIGDLAGTSRJLGEKVKSGAVTDPEBKHT-KAD 481	
DDB	519 EFQKQFDPLGNIDDS-KRSTL-LKFVTPPLPGEIERRSKGYETITLKVGV 576	
DQ	482 KLV-QL-DSANCIIDVSNSGRAKTOHLFRPPLPCTERERVQTKYEVTKUNINRY 539	
DDB	577 DKWTVKCVQDKGAVDYSNLQHASV ---GN-NOYREIRIESHLGDGDDKVFSLSGSA 630	
DQ	540 DSWK17DGA-SSTEDEDINVQRIQFIELDNAGNVTIKTEKIAKIGEGDDNVFGSGT 598	
DDB	631 NIYAGKCHVVYYDKTDGTYLTDTGKTAEGAGNYTVTRVGGDVKVLQEYVKEQEVSGK 690	
DQ	658 REEKIEYRHSSNNHHAG-YIT KDTKAVEETIGTSNDIFKGSKENDAANGGDVTDID 715	
DDB	751 GNDGNDRUYGDKGNDTLLGGNDQDOLGGDNDKLJGAVAGNN-YLN-GGDGD 801	
DQ	716 GNDGNDRUYGDKGNDTLLGGNDQDOLGGDNDKLJGAVAGNN-YLN-GGDGD 768	

Query Match 36.1%; Score 2244; DB 1; Length 1023;  
 Best Local Similarity 45.6%; No. 0.00e+00;  
 Matches 372; Conservative 202; Mismatches 209; Indels 32; Gaps 2

INFECT. IMMUN.	59:3026-3032(1991)
[2]	SEQUENCE FROM N.A.
RRP STRAIN-S	4074 / SEROTYPE 1;
RX MEDLINE: 94237497.	FREY J., HALDTHANN A., NICOLET J., GENE 142:97-102(1994).
[3]	SEQUENCE FROM N.A.
RRP STRAIN=ISOLATE CVI 13261 / SEROTYPE	JANSEN R., BRIERRE J., KAMP E.M., INFECT. IMMUN. 61:3688-3695(1993).
RX MEDLINE: 93366125.	
[4]	SEQUENCE FROM N.A.
RRP STRAIN-S	4074 / SEROTYPE 1;
RX CHANG Y., WANG Y., CHIN N.; SUBMITTED (JAN 1994) TO EMBL/GENBANK.	
CCC -1- FUNCTION: ONE OF THE VIRULENCE FACTORS WHICH HAS A STRONG HEMOLYTIC AND ALVEOLAR MACROPHAGES AND NEUTROPHILS SUBCELLULAR LOCATION: SECRETORY.	
CCC -1- DOMAIN: THE GLY-RICH REGION IS CALCIUM, WHICH IS REQUIRED FOR ACTIVITY.	
CCC -1- DOMAIN: THE THREE TRANSMEMBRANE INVOLVED IN PORE FORMATION BY APIXIA IS PARTIALLY DELETED IN TOTALLY DELETED IN SEROTYPE 3.	
CCC -1- SIMILARITY: SHOWN IS THAT OF CCC -1- SIMILARITY: TO OTHER HEMOLYSINS (STRUCTURAL TOXIN).	
CCC EMBL: X62895; G38959; -;	POTENTIAL
CCC EMBL: X68535; G505510; -;	POTENTIAL
CCC EMBL: X73117; G312899; -;	POTENTIAL
CCC EMBL: U05017; G606616; -;	POTENTIAL
CCC PROSITE: PS00310; HEMOLYSIN_CALCIUM_HEMOLYSIS: TOXIN; CYTOLYSIS; CYTOKINETIC TRANSMEMBRANE	POTENTIAL
CCC TRANSHEM 226 256	POTENTIAL
CCC TRANSHEM 297 326	POTENTIAL
CCC TRANSHEM 367 406	POTENTIAL
CCC DOMAIN 722 845	POTENTIAL
CCC REPEAT 722 727	POTENTIAL
CCC REPEAT 731 736	POTENTIAL
CCC REPEAT 740 745	POTENTIAL
CCC REPEAT 749 754	POTENTIAL
CCC REPEAT 758 763	POTENTIAL
CCC REPEAT 767 772	POTENTIAL
CCC REPEAT 776 781	POTENTIAL
CCC REPEAT 785 790	POTENTIAL
CCC REPEAT 794 799	POTENTIAL
CCC REPEAT 813 818	POTENTIAL
CCC REPEAT 822 827	POTENTIAL
CCC REPEAT 831 836	POTENTIAL
CCC REPEAT 840 845	POTENTIAL
CCC CONFLICT 217 217	AMINOACID
CCC CONFLICT 374 374	AMINOACID
CCC CONFLICT 562 562	AMINOACID
CCC CONFLICT 687 688	AMINOACID
CCC CONFLICT 1023 AA: 110193 MW: 76 SQ SEQUENCE 1023 AA: 110193 MW: 76	AMINOACID
Query Match 36.0% Score	
Best Local Similarity 45.5% Pred.	
Matches 371; Conservative 203; M	
Ddb 39 KOAGOKLILYTPKDYQAST-GSSLNLDV	
Ddb 11 KTGAKKLLIIPQNQYDEQGNGQLDLY	
Ddb 97 LGPSERGLAFAQPQDFKLNNKQNLKS	
Dy 71 IGLTERGIVVISAPODKLQIQLKT-KGAQO	

Db 157 MDLDSLRRRRNGEDVSGSELAKAGYDAAQLVDNTIASATGTVDAFAEQLGKLMAMPYTL 216  
 Qy 129 MDEALQNSN-OH---A-LAKAGLELTNSLENANSVYTLDFGEQISQFGSKLQNT 183  
 Db 217 -ALSGLASKLNLNPDLSSLAGPGFDVSGILSVSASPILSNKDAAGTAAAGIEISTKI 275  
 Qy 184 KGTGLGDKLNGGDKAGLGLDVSGLSSGATAAVLADKNASTAKVGAFFELAQV 243  
 Qy 276 LGNIGRAVSQTTIAQRVAAGLSTTAATGGLGSVVALAISPLSLNVADKFERAKOLEQY 335  
 Qy 244 VGNITRAVSSYLLAQRAVAGLSSGTGVAAITALASTVSLAISPLAFGIAKDFNHAKSLEY 303  
 Db 336 SERFKFGEYEGDSLLASFYRTGETAFAALTINISVLSARSAGVAAATGSVGAAPVAAVY 395  
 Qy 304 ABRFRKKLGYDGNLLAEYQRTGTIDASVATAINTLAAGVAAAAGSVIATSPALLY 363  
 Db 396 SAITGLISGILDASKQAIFERVATKLANKIDEWK-HGANYFENGYDARHSASFLEDTPE 454  
 Qy 364 SCITGVISTILOYSKQMFENHVANKLNHKLYEWXNNHGRNKFENGYDARYLANIQDNMK 423  
 Db 455 LJSQYINKEYSVERVVAITQQWDVNIGELACITRKSDTKSGKAYVDFREKGKLEKEPD 514  
 Qy 424 FLLNLKQEAERVIATQQWDNNNGDLAGISRGKEVLSKGKAYDAFFEGKHI-K-AD 481.  
 Db 515 RFDKVKEDPLESKIDLSSINK-TL-LKFVTPVFTAGEELRKRTGKYOYMTLFVKGK 572  
 Qy 482 KLVQ--LDSANGSIDYSNSGRAKTOQHILFRPLPPTGERVOTKGYKSYITKLINIRV 539  
 Db 573 EKWVITVGQVOSHNAIYDTNLQ-LAID-KK-GE- K-RQVTHESHLGEKNDRIVLSSGS 626  
 Qy 540 DSWKIRDGAA-SSTFDLTVNYQRIGIELDNAGNTVTKTKEKIIAKLGEDDNFVFGSGTT 598  
 Db 627 IVYAGNGHDVAYYKDITDGYJTFDGOSAQKAGEYTWTKELKADYKVLFKEYVKTODISYGR 686  
 Qy 599 EIDGGECDYDRYHSRGNYGAFTLTDATKETEQQSYTNRFVETG-KALHEYTSHTALVGN 657  
 Db 687 TCSEKLEYRDYFSPFELNGIRAKDELHSEVEILGNSNRKDKFEGSRFTDIFHGAKGDDE 746  
 Qy 658 R-EKKEYRHSN-NQHAGY-Y-TKDYLKAVEEITGTSHDIFSKSKENDAFNGDGVDT 713  
 Db 747 IYGDNDGHDLYGDGNDVIIHGGGNDHLYGGGNDRLIGGKGNN-FLN-GGDGDELQV 804  
 Qy 714 IDGNDGNDRLFGKGDDIDLGNGDDFIDGKGNDLHGGKGDDIFVRKGDGNDLITDS 773  
 Db 805 EGQYNYLGGAG-NDLIGSDGTNLFDDGGVGNDKI 838  
 Qy 774 DGNKLSFSDSNLKDUTFEKYKHNLVITNSKKEVY 808  
 Result 14  
 ID HLY\_ACTAC STANDARD: PRT: 1050 AA.  
 AC P16462;  
 DT 01-AUG-1990 (REL. 15, CREATED)  
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)  
 DE 34, LAST ANNOTATION UPDATE)  
 DE LEUKOTOXIN.  
 GN LKTA OR LTA.  
 OS ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS  
 OS PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC PASTEURILLACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 STRAIN-JP2;  
 RX MEDLINE: 89359362.  
 RA LALLY E.T., GOLUB E.E., KIEBA I.R., TAICHMAN N.S., ROSENBLUM J.,  
 RA ROSENBLUM J.C., GIBSON C.W., DEMUTH D.R.;  
 RL J. BIOL. CHEM., 264:15451-15456(1989).  
 CC FUNCTION: ONE OF THE VIRULENCE FACTORS OF A. ACTINOMYCETEMCOMITANS  
 CC MIGHT BE A CYTOTOXIN, POSSIBLY THE MEMBRANE-BOUND HEMOLYSIN.  
 CC SUBCELLULAR LOCATION: OUTER-MEMBRANE ASSOCIATED OR SECRETED (BY  
 CC SIMILARITY).

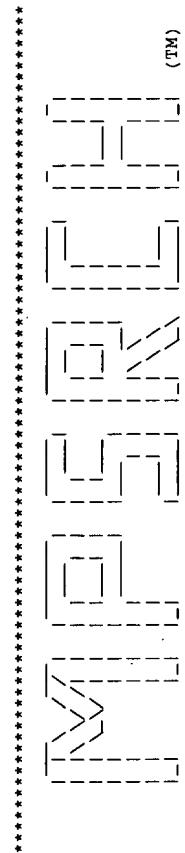
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CC -1- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING  
 CC CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC  
 CC ACTIVITY.  
 CC -1- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE  
 CC INVOLVED IN POLE FORMATION BY THE CYTOXIN (BY SIMILARITY).  
 CC -1- DISEASE: ITS TARGET CELL SPECIFICITY IS RESTRICTED TO HUMAN AND  
 CC SOME NON-HUMAN CELLS OF THE MONOCHYLOCYTIC LINEAGE.  
 CC -1- SIMILARITY: TO OTHER HEMOLYSINS OF THE RTX FAMILY (REPEAT IN THE  
 CC STRUCTURAL TOXIN).  
 DR EMBL: M27399; G141834; -.  
 DR PIR: B34345; B34345.  
 DR HSSP: P04002; 1ATF.  
 DR PROSITE: PS00330; HEMOLYSIN\_CALCIUM; CYTOKSIS; REPEAT; CALCIUM;  
 KW HEMOLYSIS; TOXIN; CYTOKSIS; CYTOKSIS; REPEAT; CALCIUM;  
 KW TRANSMEMBRANE.  
 FT TRANSMEM 339 359  
 FT TRANSMEM 408 429  
 FT TRANSMEM 477 501  
 DOMAIN 722 844  
 REPEAT 722 727  
 FT REPEAT 731 736  
 FT REPEAT 740 745  
 FT REPEAT 749 754  
 FT REPEAT 758 763  
 FT REPEAT 767 772  
 FT REPEAT 776 781  
 FT REPEAT 785 790  
 FT REPEAT 794 799  
 FT REPEAT 803 808  
 FT REPEAT 812 817  
 FT REPEAT 821 826  
 FT REPEAT 830 835  
 FT REPEAT 839 844  
 SQ SEQUENCE 1050 AA; 114194 MW; 995A56CB CRC32;  
 Query Match 34.9%; Score 2167; DB 1; Length 1050;  
 Best Local Similarity 45.8%; Pred. No. 0.00e+0;  
 Matches 190; Mismatches 212; Indels 34; Gaps 25;  
 Matches 368; Conservative 190; Missmatches 212; Indels 34; Gaps 25;  
 Db 44 KTG-KKLTYIPKNEY---KGNGLTLALKRAOKLGTEVYHEGKDGPAITNGTINTGKKL 98  
 Qy 11 KTGAKKILLYIPQNYQYDTEQGQLQDLEVKRAAELBGEVQREERNNTATAQSLGTIQTQ 70  
 Db 99 LGITERGLTLEFAPELDKWAQGNKHLNSNVG-SIGNLTKAIDKQVOSVLGLTQLAQNLTAFSGM 158  
 Qy 71 IGJTERGTVLSAPOIDKLQKTRA-QOALGSAEVSQVONANRAKTVLGSQIOTLGSVLAGM 129  
 Db 159 DLDALIKARQNGKNTVDLQAKASLNLINEGITISITNTDFTSKOLNKUGEALGQVK 218  
 Qy 130 DLDAL---QNNSN-OHA-LAKGLELTNSLLENIANSYVKTLEFGEOISQGSKLQNIK 184  
 Db 219 HFSGFDKLNPKLNPKLNQKGYGALSGYLSAISAAJLANKHADTAATKAAAELTNKVL 278  
 Qy 185 GLGTLGDKLNPKLNQKGYGALSGYLSAISAAJLANKHADTAATKAAAELTNKVL 244  
 Db 279 GNIGKATTQYLTQRAAAGLSTGPVAGLASYVSLAISPLSFLGIQKQFDARMLEYAS 338  
 Qy 245 GNTKAVSSYLLQRAVAGLSSGPVAALASTVSLAISPLSFLGIQKQFDARMLEYAS 304  
 Db 339 KREKKFGYNGDLSLGFQYKNTGADAIIITVLSLTAAGYGAASGSVLAQIGLUVS 398  
 Qy 305 ERFKLGVDGDNLLAEGORTGTIDASVTAINTALAATAGGVSAAAGSVIASPIALIVS 364  
 Db 399 AITSLSIGLDAKQAYSEHIANQDADKTKAWE-NKGKNSYENGDARHSAFLEDSLKL 457  
 Qy 365 GITGVISTLQYSQMFHEVANKHNKIVWEKNKGKNTFNGYFENGDARYLNLQDNMKF 424  
 Db 458 FNELREKVTENTLSITQGWDORIGELAGTRNGDRTOSGRAYDVYDJKKGEEELAKHSKD 517  
 Qy 425 LLNUNKEQQAERTVTAITQQWDNINQDAGISRLRGEVYDAAFEEGKHI-K-ADK 482  
 Db 518 FTKQILDPKGNIDLSGI-KGSTT-LTFNPLLTAGKEERKTRQSCKYEFIRELKVKGRT 575



Qy 256 -LAQ-R-VAAGISSTGPVRAALIASTVSLAISPLAFAGIADKEFHAKSLESYAYEREKKLYG 312  
 Db 649 EGDDALLAQLYDKTANEGAYAGSAYLSTVGAVYAAASVGAVAVYTSUJTGALNG 708  
 :||| ||| :| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 313 DGDNLAEYORGTTIDASVTAINTALAATAGVSAAAGSVIASPIALVSGITGVIST 372  
 Db 709 ILRGYQOPIEKLANDYARK1-D-ELGGP-QAYFEKLNQLARHEQFLANSGLRKMLADLQA 765  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 373 ILQYSQAMFPHVANTIHNKTEWEKNHGNYFENGDYR -- -IANDOPNMKFLLNLRK 4 30  
 Db 766 GWNASSVIGVOTETEISKSALLEAITGNAIDLNSKSYDVFNDREVQSERVAGQPVV LDVAA 824  
 | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 431 ELOAERVTIALTQQMNNIGLAGISRLGEKVLSSKAYDAFEESKHAKDLYVOLDSAN 490  
 Db 825 GGIDIASR-RGBRPAITFTPLAAPCEQRRTKGSEPTFVEJGDRWRJRDGA 883  
 | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 491 GIDVDSNSGRAKTOHLFRPLLTGTHERVQTGKYEVITKLN -NRVDSWKTDGAA 549  
 Db 884 DTIDILAKVYSQL-YD-AN-G-VYLK-HSIKLVDVIGGDGDDVYLANASRHYDGAGTNTV 938  
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 550 SSTFDJINVORIGJELDNAGNVTKTETKIAKJEGDDNVFSGTEIDGEGYDRV 609  
 Db 939 SYAALGRQDSITVA -DGER - FNYRKQNLNANYREGYATQTAYGKRTEVOYRHYE 994  
 | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 610 HYSR-SNYGALTIDATKETEQSYTVNRFETVKALHEVTSTHTALVGNEEKEYRHSN 668  
 Db 995 LARVGQVEVDLERYHQHTTGGAGNSITGWAHDNFLAGSDDRUGGAGNDTUVGEG 1054  
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 669 NQHHAGYYTKTOLKAVEETIGSHNDIFGSKENDAFNGDGVDTIDGNDNDRFGGKG 728  
 Db 1055 QNTVIGGAGDDFLQDGLGWNSNLDGGAGYDVKYVNHQPSERLERMGDTGHADL 1111  
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Qy 729 DDIDLOGNGDD-FIDG-GKGNDLHAGGKG -DDI-F -VHRKGDGN-DITDSDGNDKL 779

Search completed: Wed Dec 9 19:25:32 1998  
 Job time : 123 secs.



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MSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 19:25:49 1998; MasPar time 49.79 Seconds

936.191 Million cell updates/sec

Tabular output not generated.

Title: >US-08-455-970-12

Description: (11-36) from US08455970.PEP

Perfect Score:

Sequence: 1 MATVIDLSFPKIGAKKILY.....LSSLQFARGSOHWSYGLRPG 936

Scoring table: PAM 150  
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrembl6  
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mmc 8:sp\_organelle  
9:sp\_phage 10:sp\_plant 11:sp\_rabbit 12:sp\_unclassified  
13:sp\_vertetebrate 14:sp\_virus

Statistics: Mean 54.486; Variance 138.232; scale 0.394

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description	Pred. No.
1	2324	37.4	998	2	047461 PLASMID DNA FOR EHEC-H	0.00e+00
2	2321	37.3	998	2	047262 HEMOLYSIN.	0.00e+00
3	2307	37.1	998	2	P71223 EHEC-HEMOLYSIN.	0.00e+00
4	2207	35.5	1055	2	046715 LEUKOTOXIN.	0.00e+00
5	1758	28.3	758	2	043891 HLYA (FRAGMENT).	2.79e-17
6	1396	22.5	233	2	051865 LEUKOTOXIN A (FRAGMENT).	2.33e-17
7	1247	20.1	211	2	051867 LEUKOTOXIN A (FRAGMENT).	7.4e-173
8	1208	19.4	208	2	051868 LEUKOTOXIN A (FRAGMENT).	1.84e-166
9	1148	18.5	200	2	051866 LEUKOTOXIN A (FRAGMENT).	1.21e-156
10	887	14.3	1705	2	050517 ADENYLATE CYCLASE HEMO	2.99e-114
11	493	7.9	181	2	070070 ALPHA HEMOLYSIN (FRAGM	5.26e-52
12	492	7.9	181	2	068403 ALPHA HEMOLYSIN (FRAGM	7.48e-52
13	492	7.9	181	2	068404 ALPHA HEMOLYSIN (FRAGM	7.48e-52
14	272	4.4	219	2	P96437 EXP1.	2.02e-19
15	270	4.3	269	2	005199 SIYA PROTEIN.	3.84e-19
16	225	3.6	322	2	044223 HLYA (FRAGMENT).	4.96e-13
17	226	3.6	398	2	067179 HEMOLYSIN.	3.38e-13
18	221	3.6	835	2	056012 CELL-SURFACE ASSOCIATE	1.64e-12
19	224	3.6	997	2	044492 MANNURONAN C-5-EPIMERA	6.58e-13
20	223	3.6	997	2	044493 MANNURONAN C-5-EPIMERA	8.92e-13

#### ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	998 AA.
ID	Q47461			
AC	Q47461;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE	PLASMID-DNA FOR EHEC-HEMOLYSIN OPERON.			
GN	EHEC-HLYA.			
OS	ESCHERICHIA COLI.			
OG	PLASMID POL57.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=EDL 933;			
RX	MEDLINE; 93172659.			
RA	SCHMIDT H., BEUTIN L., KARCH H.;			
RL	INFECT. IMMUN. 63:105-106(1995).			
DR	EMBL; X86087; E152893.			
DR	PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.			
DR	PFAM; PF003533; hemolysinCabind.			
KW	PLASMID.			
SEQ	998 AA; 107032 MW; 3CCADC38 CRC32;			
Query	RSAGKKLLILLPDNY-EA-OVGGINELVKADELGTEIHTERDDTIANQFFGAEVK 85			
Match	37.4%; Score 2324; DB 2;			
Best Local Similarity	46.9%; Prod. No. 0.00e+00;			
Matches	368; Conservative 199; Mismatches 188; Indels 29; Gaps 23;			
Db	1 KTGAKKILLYPQNQYDTEQNGLQDVKRAEEELGIEQREERNNTATAGSLGTQTA 70			
Qy	11 MALDELRKQREGDISQNDIAKKSSTEELINOLVDTYSSINSTVDFSEQLNQLGFLSK 205			
Db	86 VGLTERGVATFAPQDQKLQKYGOKVGSKIGTAENVNIGKAGTVLSALONFTGIALSG 145			
Qy	71 IGLTERGIVLSPQIDKLQK-TKAQQLG-SAEVSVQNAKRTKYLGSQISLGVLAG 128			
Db	146 MDLDEAL-ONNS-N-QHALAKAGLELTNSUENIANSVTLDEFGEIQTSQFSKLQNI 183			
Qy	129 PRSSVGGKLONLPDQGDLQDYYSGILSAYSASFILGNSDAHTGKAAGIELTTQV 265			
Db	186 KGLTLEDKLKNIGGLDKAGLGLDVSGLISGATAALVLADKNASTAKVYGGFELANQV 243			
Qy	184 KGLTLEDKLKNIGGLDKAGLGLDVSGLISGATAALVLADKNASTAKVYGGFELANQV 243			

Db	266	LGNVKRASQYIQLAORMAQGLSTTAASAGLITSAVMLAISPLSFLAAADKFERAQKLESY	325		Db	146	MALDELLRKOREGEDISQNDIAKSIELINQLYDTVSSINSTVDSFSEOLNQLGSFLSSK	205
Qy	244	VGNITKAVSSILLAGRAAGLISSTGPVAAILATSTSLAISPLAFAGIADRFNHRKSLEY	303		Qy	129	MDLDEAL-ONNS-N-QHALAKAGLELTNSLIENANSVKTLDFFGEOISQFCSKLQNI	183
Db	326	SERFKLNYEGLDALLAGFHETGAIDAGLTINTVLSSAGVSASSASLIGAPISMVL	385		Db	206	PRLSVYGGKLQNLPDGLPGLDVSGILSAYSASFILGNSDAHTGTKAAGTLETTVO	265
Qy	304	AERFKLGYODGDLAELAYQRTGTDASVTAINTALAALAGVSAAAAGSVIASPTALLY	363		Db	184	KGLGTLGDKLNKGIGLKGAGLGLDVSGILSATAALVADKNASTKVGAGEFLANV	243
Db	386	SALTGTISGLEASQKAMPEHAFAERKAARFAERKAARFAERKAARFAERKAFLEDSUS	444		Qy	184	KLGKLNVEGDLALLAGFKETGADAGLTINTVLSSAGVSAAASSSLIGAPISMVL	385
Qy	364	SGITGVISTLQYSQAMFEHANKIHNVWEKKNHGKNYFENGYDARYLNLQDNNK	423		Db	266	LGNYKGKAVSOYIQLAORMAQGLSTTAASAGLITSAVMLAISPLSFLAAADKFERAQKLESY	325
Db	445	LLADFSRQHAEVERAIAITHOWHDEKEIGLAGITRNADRSOSKGKAYINYYLENGGILEAQPK	504		Qy	244	VGNITKAVSSYIQLAQRVAGLSSSTGPVALIASTVSLAISPLAFAGIADRFNHRKSLEY	303
Qy	424	FLNLNKLKEOERVIAITQQDWNNIGDLAGISRIQEKVLSLQVDAFEGRKIKAD-K	482		Db	326	SERFKLNVEGDLALLAGFKETGADAGLTINTVLSSAGVSAAASSSLIGAPISMVL	363
Db	505	EFTQQVEDPQKGTTIDS-TGNVSSV-LTFITPTPGEYERKRSQGKEYMTSLIVINGK	562		Db	386	SALTGTISGLEASQKAMPEHAFAERKAARFAERKAARFAERKAARFAERKAFLEDSUS	444
Qy	483	-LVQ-LDSANG1LTDVSNSEKAKTQHILFRTPLTPGTERREVQTGKEYTKLINIRV	539		Qy	364	SGITGVISTLQYSQAMFEHANKIHNVWEKKNHGKNYFENGYDARYLNLQDNNK	423
Db	563	DWSYKGIIKHKGIVDYSKLIQ-F-VE--K--N-TKHYQARIISPLGDDVQVYSSGAGS	615		Db	445	LLADFSRQHAEVERAIAITHOWHDEKEIGLAGITRNADRSOSKGKPYINVYLENGGLEAQPK	504
Qy	540	DSWKITD-GAASSTDPLNVRQIYIELDNAGNTTKTETKIIAKLGEQDDNNFVFGSGTI	598		Qy	424	FLLNLNKELOAERYTAITQQDWNNIGDLAGISRIQEKVLSLQVDAFEGRKIKAD-K	482
Db	616	EVFAGEGYDPVSYNKTDVGKLTDATGAPKGEYIVPKNMVGDYEVQVKEVSVYK	675		Db	505	EFTQQVEDPQKGTTIDS-TGNVSSV-LTFITPTPGEYERKRSQGKEYMTSLIVINGK	562
Qy	599	EIDGGEGYDRHYHSRGNYGALTIDATKETEQGSTVNREV-ETGFLAHETVSTTALVN	657		Qy	483	-LVQ-LDSANG1LTDVSNSEKAKTQHILFRTPLTPGTERREVQTGKEYTKLINIRV	539
Db	676	RTEKIQYRDEFERTGPGIPYDVLNHSVEELIGGHDDKEFKGGKENDIFHGADGNDYIEG	735		Db	563	DTWSVKGIIKHKGIVDYSKLIQ-F-VE--K--N-TKHYQARIISPLGDDVQVYSSGAGS	615
Qy	658	REKTEYRHSHNNOHHA-GYTTKDTLKAVEELIGTSHNDLFGSKENDAANGDGYDTIDG	716		Qy	540	DSWKITD-GAASSTDPLNVRQIYIELDNAGNTTKTETKIIAKLGEQDDNNFVFGSGTI	598
Db	736	NYGNDRLYGDGDDTISGGQDDQLEFGGSENDLKSQGDDNN-YL-TGGSDNDELQAHGAY	793		Db	616	EVFAGEGYDPVSYNKTDVGKLTDATGAPKGEYIVPKNMVGDYEVQVKEVSVYK	675
Qy	717	NDGNDRLFGKGDDIDLGGNGDDFIDGGNGDDFLHGGKNDLHGGKDDIFYHRKGDGNDIITDSGN	776		Qy	599	EIDGGEGYDRHYHSRGNYGALTIDATEQGSTVNREV-ETGFLAHETVSTTALVN	657
Db	794	NILS 797			Db	676	RTEKIQYRDEFERGGIPYDVLNHSVEELIGGHDDKEFKGGKENDIFHGADGNDYIEG	735
Qy	777	DRLS 780			Qy	658	REEKTEYRHSHNNOHHA-GYTTKDTLKAVEELIGTSHNDLFGSKENDAANGDGYDTIDG	716
RESULT	2	PRELIMINARY;	PRT;	998 AA.	Db	736	NYGNDRLYGDGDDYISGGQDDQLEFGGSENDLKSQGDDNN-YL-TGGSDNDELQAHGAY	793
ID	Q47262;	PRELIMINARY;	PRT;	998 AA.	Qy	717	NDGNDRLFGKGDDIDLGGNGDDFIDGGNGDDFLHGGKNDLHGGKDDIFYHRKGDGNDIITDSGN	776
AC	P71223;	PRELIMINARY;	PRT;	998 AA.	Db	794	NILS 797	
DT	01-FEB-1997 (TREMBLREL. 01, CREATED)				Qy	777	DKLS 780	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				RESULT	3	PRELIMINARY;	PRT;
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)				ID	P71223	PRELIMINARY;	PRT;
DE	HEMOLYSIN.				AC	P71223;	PRELIMINARY;	PRT;
GN	EHEC-HLYA.				DT	01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)		
OS	ESCHERICHIA COLI.				DT	01-FEB-1997 (TREMBLREL. 06, LAST ANNOTATION UPDATE)		
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;				DR	X94129; E218404;		
OC	ENTEROBACTERIACEAE.				DR	PF00353; hemolysin; CALCIUM;		
RN	SEQUENCE FROM N.A.				DR	PF00353; hemolysin; CabInd.		
RP	SEQUENCE FROM N.A.				GN	998 AA;	107255 MW;	7DFAA67C CRC32;
RX	MEDLINE: 9517269.				OS	ESCHERICHIA COLI.		
RA	SCHMIDT H., BEUTIN L., KARCH H.;				OS	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;		
RL	INFECT. IMMUN. 63:1155-1061(1995).				OC	ENTEROBACTERIACEAE.		
DR	EMBL: X79839; G587108; -.				RN	SEQUENCE FROM N.A.		
DR	PROSTEE: PS00330; HEMOLYSIN; CALCIUM; 2.				RP	SEQUENCE FROM N.A.		
DR	PROSTEE: PS00333; hemolysin; CabInd.				RC	STRAIN=78-92;		
SQ	SEQUENCE 998 AA;				RX	MEDLINE: 97034824.		
Query Match	37.3%; Best Local Similarity 46.8%; Matches 367; Conservative	Score 2321; Pred. No. 0.00e+00; Mismatches 188; Indels 29; Gaps 23;	Length 998; PRT; 998 AA.		RA	SCHMIDT H., KARCH H.;		
Db	29	RSAGKLLILIPDNY--EA-QGVGINELVRAADELGIEIHTERDDTAIANOFFGAAEY	85		DT	01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)		
Qy	11	KTGAKKILYIPIQYQKYGSKIGTAENYNNLKGASTVSLQNFIALSGTQIQA	70		DT	01-FEB-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)		
Db	86	VGLTERGVIAFPOLDKLQKLYQKYGSKIGTAENYNNLKGASTVSLQNFIALSG	145		DR	EHEC-HLYA.		
Qy	71	IGLTERGVIVLSPQIDKLQK-TRAGQALG-SAESIVQANKARTVSLQIAG	128		DR	PF00353; hemolysin; CabInd.		

Best Local Similarity 45.7%; Pred. No. 0.00e+00; Matches 366; Conservative 201; Mismatches 188; Indels 29; Gaps 23;

Db 29 RSAGKLLIPDNY--EA-QGYGINELVKADELGEIHRVERDDTAIAQNGFFGAEKV 85  
Qy 11 KITAKKILYIIPONQYDTEQQNGLQDLVKAEEFLGEVQRERNNTAQTSILGTQTA 70

Db 86 VGLTERGYAIFAFOLDKLUOKYVGSKIGRAENVNGLKGATGIFTALSONFTGIALSG 145  
Qy 71 IGLTERGVLSAQIDKLUQK-TKAGQALG-SAESIVQNANFARTVSGIQILGSVLAG 128

Db 146 MADELLRKQREGEDISONDIKKSSIELINOLYDVTYSSINSTYDSFSEQLNQGSPFLSK 205  
Qy 129 MDLDEAL--QNN-N-`QHALAKAGLELTNSLJENTANSVKLDFEQSISQFGSKLQNI 183

Db 206 PRUSSVGKMLQNUPDLGSLGOLDVSSILSAYSASFILGNDPAHTOTKAAGIELTQV 265  
Qy 184 KGLGTTGDKLKNQNLGDKLQAGLTDVSSILSGATAALVLDNASTAKVGGFELANQV 243

Db 266 LGNYGKAVSOYIILAORMAQSLSTAASAGLITSAVMLAISPLSFLAAADKFERRAKOLEY 325  
Qy 244 VGNITKAVSYIILAORVAQGLSTGPYAA LISTVSLAISPLAFAIGTADKFPHAKSDEY 303

Db 326 SERFKKLNEYGDALLAFAHKETCAIDAALTINTVLSVSSAGSYAASSASLIGAPISMV 385  
Qy 304 AERFKKUYGDGNLIAEYQRTGCTIDASVTAINTALAAIAGGSYAAAAGSVASPIALV 363

Db 386 SALTGTGSLILASKQAMFEHAYKFAARINWEKE-HGKKNYFENGYDARHAFLEDLS 444  
Qy 364 SGITGVISTILQYSKQAMFEHANKIHNKIVEMEKNHGKKNYFENGYDARYIANLQDNMK 423

Db 445 LIAADFSDRHOHAVERAATVQHQHDEKEPLAGLCTRADSRSQSKAYINYLNLEGGGLEAQPK 504  
Qy 424 FLINLNKEQAERTVATQQWQNNIGPLAGSRLRGKYLGSRAYDAFEERHIRAD-K 482

Db 505 EFTQOVEDPQKGTDLTS-TGNYSSV-LTFITPLFTPGBEVRKOSKGKYEMTFLYING 562  
Qy 483 -LVQ- -LDSANGLTDVNSGKAKTOHLLFRTPPLPTGEHRERVQTCRYEETKLNRV 539

Db 563 DTWSVKGKINHGVYDYSKLIQ-F-VE--K--D-TKHYQARMTSELGDKDDVYSGASS 615  
Qy 540 DSNKITD-GAASASSTEDLTNVQRIQGELDNGAVNTKETK1FAKLEGDDNFVFGSGTT 598

Db 616 EVFAGEGHDPVSYNTDVGKLTIDATGASKPGFVYPPNMGYDEVLOEVYKEQEYVGK 675  
Qy 599 EIDGEGGDVRVHSRGNNGALTIDATKTEEQGSTVNFEV-ETGKAHEVTSHTAIVGN 657

Db 676 RTEKIQYDDEFRTGIGPYDVIDLHSSVEELIGKHDEFKGKENDIFHGADGNDYIEG 735  
Qy 658 REEKIEYRHNSNQHHA-CYYTKOTLKAVEEIGTSNDIFKGSKENDAFNGDGVDTID 716

Db 736 NYGNDRLYGDDDDYISGGQDDDFLGEGSGNDKLSGGDGNNTL-TGSGSGNDFLQAHGAY 793  
Qy 717 NDGNDRLEFGKGDDDFDGGNGDDFIDGGKGNNDLHGGKGDDFVHRRKGDDNLIITSDGN 776

Db 794 NILS 797  
Qy 777 DKLS 780

RC STRAIN=JP2;  
RA KOLODRUBETZ J. , DAILEY T. , KRAIG E. ;  
RL INFECT. IMMUN. 58:920-929 (1991).  
DR EMBL; X16829; G38645; - .  
DR PROSITE: PS00330; HEMOLYSIN CALCIUM; 3.  
DR PFAM: PF0053; hemolysin cabin.  
SQ SEQUENCE - 1055 AA; 113853 MW; 93491AFF CRC32;

Query Match 35.5%; Score 2207; DB 2; Length 1055;  
Best Local Similarity 46.1%; Pred. No. 0.00e+00;  
Matches 371; Conservative 189; Mismatches 210; Indels 34; Gaps 25;

Db 4 KTG-KKUTLYTPRKNY---KGNGLTALIRAAQKLGJTEVHEKGKDGPALTGILNTGKL 98  
Qy 11 KTGAKKILLYPQNYQDTEQNGLQDLVKAEEFLGEVQERNNNTAQTSILGTQTA 70

Db 9 LGLTERGLTFAPELQKWIQGNKHLNSVGSTGNLTKAIDKVQSVLGTLOAFLNTAFTSGM 158  
Qy 71 IGLTERGLTVAISPLAQPQDILQTKA-GOALSAAESTVQNANFARTVSGIQSISLGSVLAGM 129

Db 159 DDLALKARQNCNKNTDVQKLAKSALNLINELIGTISSTINNDTFSKQNLKGEALQVK 218  
Qy 130 DLDEAL--QNNN-QHA-LAKAGLELTNSLJENTANSVKLDFEQSISQFGSKLQNI 184

Db 219 HGSF9GDKLKNLPKLNQNLKGKLGALSGVLSAISALLANKEADATKAAAELTNKVL 278  
Qy 185 GJGTGDKLKNQNLKGKLGIVSLGSLCATAALVADNASTAKVGGFELANQV 244

Db 279 GNIGKALTQYLTQARAAGAQLSTGPYAGLIASSVSLAISPLSFLGTAKQFDARMLEEYS 338  
Qy 245 GNTKAVSYTTLQSYQRYAAGLSSTGPYAA LISTVSLAISPLAFAIGTADKFENHAKSLEYA 304

Db 339 KRFKEKGNGDSLQGYKNTGIAADATTINTVLSAIAAGGAAGASGSLSVAGPIGLVS 398  
Qy 305 ERFKKUYGDGNLIAEYQRTGCTIDASVTAINTALAAIAGGSYAAAAGSVIASPTALV 364

Db 399 ATSSLISGILDASKQAVFETIANLQDAKIKAWE-NYKGKNYFENGYDARHASFEDLSKL 457  
Qy 365 GTITGVISTILQYSKQAMFEHANKIHNKIVEMEKNHGKKNYFENGYDARYIANLQDNMK 424

Db 458 FNELREKXYTENLISLTIQOQWDORIGELAGTRGRDIOQSKAYVKEVNNHGKKNYFENGYDARYIANLQDNMK 517  
Qy 425 LUNLNKEQAERTVATQQWQNNIGPLAGSRLRGKYLGSRAYDAFEERHIRAD-K-ADK 482

Db 518 FTQIQLDPIKGNDLSC1-KGSTT-LTFINPLTACKERKTRQSKYBFETLKVKGRT 575  
Qy 483 LV-Q-LDSANGLTDVNSGKAKTOHLLFRTPPLPTGEHRERVQTCRYEETKLNRV 539

Db 576 D-WVKCVPNSVQYDFNSNLIOH-AVTRDN -KVL--EARLJANIGAKDDYVFYGSST 628  
Qy 540 DSWKITDQASS-TFDLINVQIGELDNNAGNVTKTKEVINKLGEGDNNFVQSGST 598

Db 629 IYNAGDGYDWDYDSKGRGALTIDGRNATKAGQKYVERDLSCTQVLOETVSKQETKRGKV 688  
Qy 599 EIDGEGGDVRVSYRGNQAU-TIDATEKEDQSYTNRFVENGKALHEVTSHTAIVGNR 658

Db 689 TDLEWYKLDYIYTNGKFKAHDELNSEEIGSTLRDKFVGSKENDUVFHGDLLY 748  
Qy 659 EKIEYRHNS-NQHHA -GYTKDTLKAVEETGTSNDIFKGSKENDAFNGDGVDTID 715

Db 749 GYDGDDRYDQGNDNGNDEIHGGQGNDKLYGAGNDLRFGEYGNN-YLD-GCEGDDHLECGNG 806  
Qy 716 GNDGNDRFFGGDDILGGNGDFIDGGKNDLHGGKGDDFVHRRKGDDNLIITDSG 775

Db 807 SDTRLRGSSGNDK-L-FGNQGDDL 828  
Qy 776 NDKLFSDSNLKDLTFFRVKHNLV 799

RESULT 5  
ID Q46716 PRELIMINARY;  
AC Q46716; PRT; 758 AA.  
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
DT 01-JUN-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE LEUROTOXIN.  
GN LKTA.  
OS ACTINOBACILLUS ACTINOMYCETOMOMTANS.  
OC PROBACOPA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
OC PASTEURILLACEAE.  
RN [1] SEQUENCE FROM N.A.  
RP



RESULT	8	PRELIMINARY;	PRT;	208 AA.
ID	Q51868;			
AC	Q51868;			
DT	01-NOV-1996	(TREMBREL_01, CREATED)		
DT	01-JUN-1996	(TREMBREL_01, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998	(TREMBREL_06, LAST ANNOTATION UPDATE)		
DE	LEUKOTOXIN A (FRAGMENT).			
OS	PASTURELLA HAEMOLYTICA.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; PASTURELLACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=T4 SEROTYPE;			
RA	LAINSON A.F.; AITCHISON K.D., DONACHIE W.;			
RL	SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.			
DR	EMBL: 22885; G31831; -			
DR	PROSITE: PS00330; HEMOLYSIN CALCIUM; 1.			
DR	PFAM: PF00353; hemolysinCabinD.			
FT	NON-TER 1			
SQ	SEQUENCE 208 AA; 22803 MW; A8C5DB0F CRC32;			
Query Match	19.4%	Score 1208; DB 2; Length 208;		
Best Local Similarity	82.2%	Pred. No. 1.8e-166;		
Matches	171;	Conservative 21; Mismatches 16; Indels 0; Gaps 0		
Db	1 GNDRLFGKGKDDIDGGNGDDFDGKGKNDLHGGKDDIFVHRODGND SITESSGNDK 60			
Qy	719 GNDRLFGKGKDDIDGGNGDDFDGKGKNDLHGGKDDIFVHRODGND SITESSGNDK 778			
Db	61 LSFSDSNKLDTFEKVNHLVTINTKOEKVTONWREAFAKTRINYVATRDKKEEII 120			
Qy	779 LSFSDSNKLDTFEKVNHLVTINTKOEKVTONWREAFAKTRINYVATRDKKEEII 838			
Db	121 QGNERITISKYDKEIKGKGKIDSLSLDSQVYDNOLKKYSRDASNSDLKLISSAFASTS 180			
Qy	839 QGNERITISKYDDELIANGNGKTQDELSKVVDNYELLIKHSRNVTNSDLKLISSAFASTS 898			
Db	181 SNDRSRVNIASPTSMLDPSLSSIOFARA 208			
Qy	899 SNDRSRVNIAPTSMLDQSLSSIOFARG 926			
RESULT	9	PRELIMINARY;	PRT;	200 AA.
ID	Q51866;			
AC	Q51866;			
DT	01-NOV-1996	(TREMBREL_01, CREATED)		
DT	01-NOV-1996	(TREMBREL_01, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998	(TREMBREL_06, LAST ANNOTATION UPDATE)		
DE	LEUKOTOXIN A (FRAGMENT).			
OS	PASTURELLA HAEMOLYTICA.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; PASTURELLACEAE.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=T4 SEROTYPE;			
RA	LAINSON A.F.; AITCHISON K.D., DONACHIE W.;			
RL	SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.			
DR	EMBL: 22886; G31827; -			
DR	PROSITE: PS00330; HEMOLYSIN CALCIUM; 1.			
DR	PFAM: PF00353; hemolysinCabinD.			
FT	NON-TER 1			
SQ	SEQUENCE 200 AA; 21986 MW; 172FA6E4 CRC32;			
Query Match	18.5%	Score 1148; DB 2; Length 200;		
Best Local Similarity	81.5%	Pred. No. 1.21e-156;		
Matches	163;	Conservative 21; Mismatches 16; Indels 0; Gaps 0		
Db	1 KGDDIDGGNGDDFDGKGKNDLHGGKDDIFVHRODGND SITESSGNDKLFSESDNL 60			
Qy	727 KGDDIDGGNGDDFDGKGKNDLHGGKDDIFVHRODGND SITESSGNDKLFSESDNL 786			
Db	61 KDFFEKFVNHLVTINTKOEKVTONWREAFAKTRINYVATRDKKEEII QGNGERIT 120			

Qy	787	KDLTEPKVHNLTNSKKERKVTONWFRDAEVPNKTDKRKEETIGONGRIT	846
Db	121	SKQVDLIEKGKGDLKSDSLSQVNTQYOLKYSRDAKSNSLDKLSSASAFTSSNSDNRNVL	180
Qy	847	SKQVDLIAKGNGKTDQDELSKVKVNTQYELLKHSKVNTNSLDKLSSAFTSSNSDNRNVL	906
Db	181	ASPTMLDPLLSSTOFARAA 200	
Qy	907	VAPTSMDQSLSLQFARGS 926	
	RESULT 10	PRELIMINARY;	
	ID 005179	PRT: 1705 AA.	
	AC		
	DT 005179; 01-JUL-1997 (TREMBLREL. 04, CREATED)		
	DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)		
	DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)		
	DE ADENYLATE CYCLASE HEMOLYSIN.		
	GN CYAA.		
	OS BORDETELLA BRONCHISEPTICA.		
	OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;		
	OC ALCALIGENACEAE.		
	RN [1]		
	RP SEQUENCE FROM N.A.		
	RC STRAIN=CIP 9.73;		
	RX MEDLINE: 96009899.		
	RA BETSOU F.; SISHEIRO O.; DANCHIN A., GUIZO N.;		
	RA GENE 162:165-166(1995).		
	RL RN [2]		
	RP SEQUENCE FROM N.A.		
	RC STRAIN=CIP 9.73;		
	RA DANCHIN A.;		
	RA SUBMITTED (SEP-1994) TO EMBL/GENBANK/DDJB DATA BANKS.		
	RL RN [3]		
	RP SEQUENCE FROM N.A.		
	RC STRAIN=CIP 9.73;		
	RA DANCHIN A.;		
	RA SUBMITTED (APR-1997) TO EMBL/GENBANK/DDJB DATA BANKS.		
	RL DR EMBL: 237112; B310699; -		
	DR PROSTME: PS003336; HEMOLYSIN_CALCIUM; 4.		
	DR PFAM: PF00353; hemolysin_cabn.		
	SEQUENCE 1705 AA; 177249 MN; 452163B0 CRC32;		
	Score 887; DB 2; Length 1705;		
	Best Local Similarity 31.8%; Pred. No. 2.99e-114;		
	Matches 190; Conservative 165; Mismatches 212; Indels 30; Gaps		
	Query Match 14.38; Score 887; DB 2; Length 1705;		
	Best Local Similarity 31.8%; Pred. No. 2.99e-114;		
	Matches 190; Conservative 165; Mismatches 212; Indels 30; Gaps		
Db	530	GGFGYAGGAMALGGGI-GAYGAGMSLTD-DAPAGQXAAAGAEIAQLQTGTVLAEASSIAL 587	
Qy	197	GGLDRAFTGLDVISGLSGATAALVADKNASTAKVGVQVNITKAQVSSY-I 255	
Db	588	ALAARGVGTQVAGASAGAAAGALAALPMTTYGLVQOQSHYADQDLKLAQESSAYY 647	
Qy	256	-LAQ-R-VAAGLSSGPVAALIYSTSLAIFIAGDENHAKSLESYAFRKFLKGY 312	
Db	648	EGDDALIAQLYRDKTAEGAVAGVSAYLSTVGAAVSTAAAASVVGAPAVVTSUTLGALN 707	
Qy	313	DGDNLIAEYORGTTIDASVTAINTALAAIAGGSAAAAGSVTASPIALLYSGITGVIST 372	
Db	708	ILRGWQPIEKLANDYARKI-D-EUJGP-OAYFEKRNQARHEQLRNLGKMLADLQA 764	
Qy	373	ILQYSSQAMEHVANKIHKVWEKNNHGKNYFENGYDARY--LANQDNMKFLNLNK 430	
Db	765	GWNAASVIGVOTTEISKSALEAATGNAIDLNSKFDVDRFIQGERVAGQPVV-LDVA 823	
Qy	431	ELQAEVRIATQQQWNIGNDIAGSISLGEKVLSGRAYVDAEKGKHIAKDSLQNSAN 490	
Db	824	GGDIDASR-KGERPALTIFITPLAAPPGEQRRRTKGKSEFTFVEVKGQDKMRIRDGAA 882	
Qy	491	GLIDVNSNGKAKTOHILFRTPLPSTEHERVQTYGKEYLTKLNI-NRVDWKITDGA 549	
Db	883	DTIDIAKVVSQL-VD-AN-G-VLK HSIKLEVIGGGDDVVVLANASIRHYOGAGNTV 937	



AC P96437; 1997 (TREMBLREL. 03; CREATED)  
DT 01-MAY-1997 (TREMBLREL. 03; LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TREMBLREL. 06; LAST ANNOTATION UPDATE)  
DE SINORHIZOBIUM MELILOTTI.  
OC EUBACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE;  
OC SINORHIZOBIUM.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAINERM2011;  
RX MEDLINE; 97175570.  
RA BECKER A., RUEBERG S., KOESTER H., ROXLAU A.A., KELLER M., IVASHINA T.,  
RA CHENG H., WALKER G.C., PUENHLER A.;  
RL J.BACPEROL, 179:1375-1384(1997).  
DR EMBL: Z79692; E23873; -.  
DR PROSITE; PS00330; HEMOLYSIN\_CALCIUM; 4.  
DR PFAM; PF00353; hemolysinCaind.  
SQ SEQUENCE 219 AA; 22116 MW; A6EF047F CRC32;

Query Match 4.4%; Score 272; DB 2; Length 219;  
Best Local Similarity 46.5%; Pred. No. 2.02e-19;  
Matches 47; Conservative 21; Mismatches 32; Indels 1; Gaps 1;

Db 63 GTDVLYGENGNIDLVGSGGDDLLYQDNGNDLILGGAGSDFLLGGRNDVLDAGNDVID 122  
Qy 683 AVEELITTSNHNIFKGSKENDFNGDQVDTIDGNDNDRFFGKDDIDLGNGDDFDID 742  
Db 123 GGAGSDLLAGGGQSDIIFYFDGGGGNDVLDLDFPGEDYLQIS 163  
Qy 743 GKGNDLHGGKDDIFVHRKGNDLITD-SDGNDRLSFS 782

RESULT 15  
ID 005199 PRELIMINARY; PRT; 269 AA.  
AC C05199;  
DT 01-JUL-1997 (TREMBLREL. 04; CREATED)  
DT 01-JUL-1997 (TREMBLREL. 04; LAST SEQUENCE UPDATE)  
DT 01-AUG-1998 (TREMBLREL. 07; LAST ANNOTATION UPDATE)  
DE SILVA PROTEIN.  
GN  
OC SINORHIZOBIUM MELILOTTI.  
OC EUBACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE;  
OC SINORHIZOBIUM.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAINEFBL;  
RA LLORET J., WULFF B.B.H., RUBIO J.M., DOWNE J.A., BONILLA I.,  
RA RIVILLA R.;  
RL APPL. MICROBIOL. 64:1024-1028(1998).  
DR EMBL: Y08703; F233909; -.  
DR PROSITE; PS00330; HEMOLYSIN\_CALCIUM; 4.  
DR PFAM; PF00353; hemolysinCaind.  
SQ SEQUENCE 269 AA; 27870 MW; 6FC23DBA CRC32;

Query Match 4.3%; Score 270; DB 2; Length 269;  
Best Local Similarity 46.5%; Pred. No. 3.84e-19; Length 269;  
Matches 46; Conservative 22; Mismatches 29; Indels 2; Gaps 2;

Db 115 DVLHGENGNDLVGGSGDDLLYQDNGNDLILGGAGSDFLLGGRNDVLDAGNDVID 174  
Qy 686 EII-GTSHNDIKGSKENDAFNGDGVDTIDNDGNDRLFGKGDDIDLGNGDDFDGG 744  
Db 175 SGSDLLAGQGSDIIFYFDGGGGNDVLDFTPBDVQIS 213  
Qy 745 KGNDLHGGKDDIFVHRKGNDLITD-SDONDKLSSFS 782

Search completed: Wed Dec 9 19:30:04 1998  
Job time : 255 secs.



title: >US-08-455-970-12  
description: (1-936) from US08455970.pop

Perfect Score: 6217  
Sequence: 1 MATVIDLSFPKGTGAKKILY.....  
scoring table: PAM 150

· searched: 77309 seas. 7078906 residues · Gap 11

post-processing: Minimum Match 0% Listing first 45 summaries

database: a-issued 215 count 8 notes 2000 21

statistics: Mean 34.902; Variance 201.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	No.	Query			Length	DB	ID	Description	Pred. No.
		Score	Match	%					
1	6217	100.0	936	1	US-08-455-		Sequence 12, Applicatio	0.00e+00	
2	6135	100.0	977	1	US-08-387-		Sequence 8, Applicatio	0.00e+00	
3	6135	98.7	1069	1	US-07-777-		Sequence 9, Applicatio	0.00e+00	
4	6135	98.7	1069	1	US-08-170-		Sequence 4, Applicatio	0.00e+00	
5	6128	98.6	926	3	547657-3		Patent No. 547657.	0.00e+00	
6	6128	98.6	926	1	US-08-387-		Sequence 6, Applicatio	0.00e+00	
7	6128	98.6	926	1	US-07-108-		Sequence 2, Applicatio	0.00e+00	
8	6128	98.6	926	1	US-08-455-		Sequence 2, Applicatio	0.00e+00	
9	6128	98.6	943	1	US-08-455-		Sequence 10, Applicatio	0.00e+00	
10	6128	98.6	951	1	US-08-455-		Sequence 14, Applicatio	0.00e+00	
11	6057	97.4	1098	1	US-08-170-		Sequence 2, Applicatio	0.00e+00	
12	6057	97.4	1098	1	US-07-777-		Sequence 7, Applicatio	0.00e+00	
13	4925	97.9	934	1	US-08-215-		Sequence 80, Applicatio	0.00e+00	
14	25656	41.3	1244	2	PCT-US93-1		Sequence 2, Applicatio	6.12e-17	
15	2239	36.0	544	1	US-08-387-		Sequence 10, Applicatio	1.35e-15	
16	2167	34.9	1403	1	US-07-908-		Sequence 3, Applicatio	3.06e-14	
17	2160	34.7	1334	3	547657-1		Patent No. 547657.	1.01e-14	
18	1758	28.3	758	1	US-08-558-		Sequence 2, Applicatio	7.08e-11	
19	1758	28.3	758	1	US-08-526-		Sequence 2, Applicatio	7.08e-11	
20	1758	28.3	758	1	PCT-US93-0		Sequence 2, Applicatio	7.08e-11	
21	896	14.4	1489	3	5183745-2		Patent No. 5183745.	2.18e-54	
22	896	14.4	1794	3	5183745-6		Patent No. 5183745.	2.18e-54	
23	6133	26.6	613	1	US-08-722-		Sequence 3, Application	1.23e-02	

24	2.3	20	3	5476657-6	Patent No.	5476657-
140	2.3	20	1	US-07-908-	Sequence 5,	Applicatio
140	2.3	20	1	US-07-777-	Sequence 4,	Applicatio
140	2.3	20	1	US-08-100-	Sequence 6,	Applicatio
140	2.3	1536	1	US-08-302-	Sequence 2,	Applicatio
28	133	2.1	1536	1	US-08-038-	Sequence 2,
29	133	2.1	1536	1	US-08-393-	Sequence 5,
30	133	2.1	2035	2	PCT-US93-1	Sequence 5,
31	133	2.1	2035	2	US-08-046-	Sequence 5,
32	133	2.0	2026	1	US-08-194-	Sequence 7,
33	123	2.0	1026	1	US-08-062-	Sequence 5,
34	119	1.9	341	1	PCT-US94-0	Sequence 5,
35	119	1.9	341	1	US-08-891-	Sequence 5,
36	119	1.9	341	2	PCT-US96-0	Sequence 5,
37	119	1.9	341	1	US-07-661-	Sequence 2,
38	117	4.33	230	1	US-07-118-	Sequence 3,
39	110	1.8	230	1	US-07-845-	Sequence .5,
40	113	1.8	730	1	US-07-846-	Sequence 5,
41	113	1.8	730	1	US-08-446-	Sequence 15,
42	106	1.7	37	1	US-07-609-	Sequence 78,
43	105	1.7	572	1	US-08-765-	Sequence 2,
44	105	1.7	652	2	PCT-US95-1	Sequence 2,
45	107	1.7	746	2	US-08-771-	Applicatio

ALIGNMENTS

RESULT 1 ID US-08-455-970A-12 STANDARD; PRT; 936 AA

XX  
AC  
XX

Sequence 12, Application US/08455970A  
XX  
CC

CC Patent No. 5708155  
CC GENERAL INFORMATION:  
CC APPLICANT: POTTER, ANDREW A.

CC APPLICANT: REDMOND, MARK J.  
CC APPLICANT: HUGHES, HUW P.A.  
CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY

CC TITLE OF INVENTION: CHIMERAS  
CC NUMBER OF SEQUENCES: 15  
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: REED & ROBINS  
CC STREET: 285 HAMILTON AVENUE, SUITE 200  
CC CITY: NEW YORK, NY 10001

CC CC CC  
CITY : PALO ALTO  
STATE : CALIFORNIA  
COUNTRY : UNITED STATES OF AMERICA

CC ZIP: 94301 COMPUTER READABLE FORM:  
CC MEDIUM TYPE: FLOPPY disk  
CC

CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patient In Release #1.0. Version #

CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/455, 970A  
CC FILING DATE: 21-Nov-1905  
CC

CC CC CC  
FILING DATE: 31 MAY 1999  
CLASSIFICATION: 4.24  
PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/9960, 932  
CC FILING DATE: 14-OCT-1992  
CC ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 0001-0016 10

CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 327-3400  
CC TELEFAX: (415) 327-1231  
CC INFORMATION FOR SEQ ID NO: 12:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 936 amino acids

CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 SQ SEQUENCE 936 AA; 100529 MW: 4311495 CN;

Query Match 100.0%; Score 6217; DB 1; Length 936;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKAKIIYIPQNYQDTEQGLDLYKAEEELGIEVQREERNNTIATA 60  
 Qy 1 MATVIDLSFPKAKIIYIPQNYQDTEQGLDLYKAEEELGIEVQREERNNTIATA 60

Db 61 QTSLGTTQTAIGLTERRIVLSPQIDKLQLKTKAQCAQLSAESIVQANAKTLYSGIOS 120  
 Qy 61 QTSLGTTQTAIGLTERRIVLSPQIDKLQLKTKAQCAQLSAESIVQANAKTLYSGIOS 120

Db 121 IGSVLAGMDLEALQNSNQHALAKAGLETLNSLIENANSVKTLDERGEQISOFGSKL 180  
 Qy 121 IGSVLAGMDLEALQNSNQHALAKAGLETLNSLIENANSVKTLDERGEQISOFGSKL 180

Db 181 QNIKGIGLTGDKLNKIGLDAKGLDVISGLSATAALVLADKNASTAKKVAGFELA 240  
 Qy 181 QNIKGIGLTGDKLNKIGLDAKGLDVISGLSATAALVLADKNASTAKKVAGFELA 240

Db 241 NQVGNITKAVSYTIAQRYAAGLSSGTGPVAAILASTVSLAISPLAFAGTADKFNHAKSL 300  
 Qy 241 NQVGRITKAVSYTIAQRYAAGLSSGTGPAALASTVSLAISPLAFAGTADKFNHAKSL 300

Db 301 ESYAERFKKLGYDGDNLLAEBYQRGRTGTDASVTAINTALAAIAGGYSAAAAGSYIASPIA 360  
 Qy 301 ESYAERFKKLGYDGDNLLAEBYQRGRTGTDASVTAINTALAAIAGGYSAAAAGSYIASPIA 360

Db 361 LIVSGTGTVISTLQYSQAMEHYANKIHNKIVWEKNNHGKNFENGYDARYLANLQD 420  
 Qy 361 LIVSGTGTVISTLQYSQAMEHYANKIHNKIVWEKNNHGKNFENGYDARYLANLQD 420

Db 421 NMKFLNLNKELQAERVIATQQQWDNNIGDLAGLSRLGKVKLSSKAYDAFEEGKHKA 480  
 Qy 421 NMKFLNLNKELQAERVIATQQQWDNNIGDLAGLSRLGKVKLSSKAYDAFEEGKHKA 480

Db 481 DKLVQLDSANGSIDVSNSGAKTOHILFRPLTPGTHERVOTGKYEYITKLINRVD 540  
 Qy 481 DKLVQLDSANGSIDVSNSGAKTOHILFRPLTPGTHERVOTGKYEYITKLINRVD 540

Db 541 SWKITDGAASSTFDLNVQIRGTYIELDNAGNVTKETKIAKGEGDDNVFGSGTBDI 600  
 Qy 541 SWKITDGAASSTFDLNVVQIRGTYIELDNAGNVTKETKIAKGEGDDNVFGSGTBDI 600

Db 601 DGEGYDRVHSRGNGNALTIDATEKTEQSYTVNRFETGKALHEVTSTHTALVGNEE 660  
 Qy 601 DGEGYDRVHSRGNGNALTIDATEKTEQSYTVNRFETGKALHEVTSTHTALVGNEE 660

Db 661 KIEYRHSNNOHHAGYTKDTLKAVEELIGTSHNDIFGSKENDAFAFGNGDVTIDGNDGN 720  
 Qy 661 KIEYRHSNNOHHAGYTKDTLKAVEELIGTSHNDIFGSKENDAFAFGNGDVTIDGNDGN 720

Db 721 DRLEFGSKGDDIDLGGNGDDFIDGGKNDLHLHGKGDDDFHRKGDDIDLTDSDGNDKLS 780  
 Qy 721 DRLEFGSKGDDIDLGGNGDDFIDGGKNDLHLHGKGDDDFHRKGDDIDLTDSDGNDKLS 780

Db 781 FDSNLUKDLPEVKRNHLVITNSKEKVTIONWFREADFAKEPVYKATKDEKEEITGQ 840  
 Qy 781 FDSNLUKDLPEVKRNHLVITNSKEKVTIONWFREADFAKEPVYKATKDEKEEITGQ 840

Db 841 GERITSKVOYDDIAKGNGKTIODLESKVVYDNEYELLKHSKRNNTNSLKLSSVSAFTSSN 900  
 Qy 841 GERITSKVOYDDIAKGNGKTIODLESKVVYDNEYELLKHSKRNNTNSLKLSSVSAFTSSN 900

Db 901 DSRNVLVAPTSMSLQDSLSSQFARGSQHWSYGLRPG 936  
 Qy 901 DSRNVLVAPTSMSLQDSLSSQFARGSQHWSYGLRPG 936

RESULT 2 STANDARD; PRT; 977 AA.  
 ID US-08-387-156-8 XX AC xxxx  
 Sequence 8, Application US/08387156  
 CC Sequence 8, Application US/08387156  
 CC Patent No. 5723129  
 CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC APPLICANT: REDMOND, MARK J.  
 CC APPLICANT: HUGHES, HOW P.A.  
 CC TITLE OF INVENTION: GORB-LEUKOTOXIN CHIMERAS  
 CC NUMBER OF SEQUENCES: 28  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: REED & ROBINS  
 CC STREET: 635 BRYANT STREET  
 CC CITY: PALO ALTO  
 CC STATE: CALIFORNIA  
 CC COUNTRY: UNITED STATES OF AMERICA  
 CC ZIP: 94101  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: FLOPPY DISK  
 CC COMPUTER: IBM PC COMPATIBLE  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PATENT RELEASE #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/387-156  
 CC FILING DATE: 10-FEB-1995  
 CC CLASSIFICATION: 424  
 CC PRIOR APPLICATION DATA:  
 CC ATTORNEY / AGENT INFORMATION:  
 NAME: ROBINS, ROBERTA L.  
 REGISTRATION NUMBER: 33,208  
 CC FILING DATE: 14-OCT-1992  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US/07/79,171  
 CC FILING DATE: 16-OCT-1991  
 CC TELEPHONE: (415) 617-8999  
 CC TELEFAX: (415) 327-3331  
 CC INFORMATION FOR SEQ ID NO: 8:  
 CC SEQUENCE CHARACTERISTICS:  
 LENGTH: 977 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 SQ SEQUENCE 977 AA; 104869 MW; 4761174 CN;

Query Match 100.0%; Score 6217; DB 1; Length 977;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 MATVIDLSFPKAKIIYIPQNYQDTEQGLDLYKAEEELGIEVQREERNNTIATA 60  
 Qy 1 MATVIDLSFPKAKIIYIPQNYQDTEQGLDLYKAEEELGIEVQREERNNTIATA 60  
 Db 121 ILGSVLAGMDLEALQNSNQHALAKAGLETLNSLIENANSVKTLDERGEQISOFGSKL 180  
 Qy 121 ILGSVLAGMDLEALQNSNQHALAKAGLETLNSLIENANSVKTLDERGEQISOFGSKL 180  
 Db 181 QNIKGIGLTGDKLNKIGLDAKGLDVISGLSATAALVLADKNASTAKVYAGFELA 240

TESTSUIT 3  
D D US-07-777-715-9  
X X STANDARD:  
C C PRT;  
XXXXXX 1069 AA.

Sequence 9, Application US/07777715  
 Sequence 9, Application US/07777715  
 Patent No. 5273889

GENERAL INFORMATION:  
 APPLICANT: Porter, Andrew  
 APPLICANT: Campos, Manuel  
 APPLICANT: Hughes, Huw P.A.  
 TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS AND USES THEREOF  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Morrison & Foerster  
 STREET: 545 Middlefield Road, Suite 200  
 CITY: Menlo Park

Db 361 LIVSGITGVISTILQYSKOMFEHYANKIHKIVEKNNKGKNYENGDARYLNLQD 4.20  
 Qy 361 LIVSGITGVISTILQYSKOMFEHYANKIHKIVEKNNKGKNYENGDARYLNLQD 4.20  
 Db 4.21 NMKFPLINLNKLQAERVIATQQWNINNIGLAGISRLGEVKLGGAYVDAFEGKHKA 4.80  
 Qy 4.21 NMKFPLINLNKLQAERVIATQQWNINNIGLAGISRLGEVKLGGAYVDAFEGKHKA 4.80  
 Db 4.81 DKLVQLDSANGIDVNSGRAKTOHQHFLRPLPTGEHRVQTGKVEYITKLNINRVD 5.40  
 Qy 4.81 DKLVQLDSANGIDVNSGRAKTOHQHFLRPLPTGEHRVQTGKVEYITKLNINRVD 5.40  
 Db 5.41 SWKITGAASTEDLINVQIGIELDNAGNTKTAKLGDDNDNVFGSGTEI 6.00  
 Qy 5.41 SWKITGAASTEDLINVQIGIELDNAGNTKTAKLGDDNDNVFGSGTEI 6.00  
 Db 6.01 DGGEYDRVHSRGNTGALTIDATKTEOGSYTVNRREVETGALKHEVTSHTALGVNRE 6.60



RESULT 5  
ID 5476657-3 STANDARD; PRT; 1003 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Patent No. 5476657.  
XX  
CC Patent No. 5476657.  
CC APPLICANT: POTTER, ANDREW A.  
CC TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN COMPOSITIONS AND USES THEREOF  
CC NUMBER OF SEQUENCES: 8  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/15, 537  
CC FILING DATE: 09-FEB-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 504, 850  
CC FILING DATE: 05-APR-1990  
CC APPLICATION NUMBER: 335, 018  
CC FILING DATE: 07-APR-1989  
CC LENGTH: 926  
SEQ ID NO:3:  
CC SEQUENCE 1003 AA; 107828 MW; 5444703 CN;  
SQ

Query Match 98 6% Score 6128; DB 3; Length 926;  
Best Local Similarity 100.0%; Pred. No. 0.00e+0;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSPPKTGAKKILLYIPQNYQDTEQNGQLDLYKAABELGIVQRERNNIATA 60  
Qy 1 MATVIDLSPPKTGAKKILLYIPQNYQDTEQNGQLDLYKAABELGIVQRERNNIATA 60  
Db 61 QTSLGTQTAIGLTERGIVLSPAPOIDKLQLQTKTQAQGLSAEVQVANKAKTVLGSQS 120  
Qy 61 QTSLGTQTAIGLTERGIVLSPAPOIDKLQLQTKTQAQGLSAEVQVANKAKTVLGSQS 120  
Db 121 LGSVLAGMDLDEALONNSNQHALAKAGILENTSLIENTANSYKTLDEFGEIQSFGSKL 180  
Qy 121 LGSVLAGMDLDEALONNSNQHALAKAGILENTSLIENTANSYKTLDEFGEIQSFGSKL 180  
Db 181 QNIKGIGTGDKLKNIGGLDKAGLGLDVSGLSGATAYLVADKNASTAKVGAGFPLA 240  
Qy 181 QNIKGIGTGDKLKNIGGLDKAGLGLDVSGLSGATAYLVADKNASTAKVGAGFPLA 240  
Db 241 NQVGNITKAVSSYLAQRVAGLUSTGPVALIYSTSLAISPLAFAGIAKDNHAKSL 300  
Qy 241 NQVGNITKAVSSYLAQRVAGLUSTGPVALIYSTSLAISPLAFAGIAKDNHAKSL 300  
Db 301 ESYAERFKKLGYDGNLILAEGYORGTTGTDASVTAINTALAAIAGGVSAAAAGSVIASPIA 360  
Qy 301 ESYAERFKKLGYDGNLILAEGYORGTTGTDASVTAINTALAAIAGGVSAAAAGSVIASPIA 360  
Db 361 LIVSGITGVISTLQYSKOMFEVANKAKHNKIVWEVKNHGANFENGDAYRLANLQD 420  
Qy 361 LIVSGITGVISTLQYSKOMFEVANKAKHNKIVWEVKNHGANFENGDAYRLANLQD 420  
Db 421 NMKFILNLNLKEQVRVIAITQQWDNNIGDLAGISRGKAVDFEGKHika 480  
Qy 421 NMKFILNLNLKEQVRVIAITQQWDNNIGDLAGISRGKAVDFEGKHika 480  
Db 481 DKLYOLDSANGIIDVSNSGKAKTOHILFRTPLJPGTETRERYOTGKEYTTKLININVD 540  
Qy 481 DKLYOLDSANGIIDVSNSGKAKTOHILFRTPLJPGTETRERYOTGKEYTTKLININVD 540  
Db 541 SWKITDGAASSTEDLTNYQIGLELDNAGNVTKTKERIKAALKGEGDNNFTVSGCTEI 600  
Qy 541 SWKITDGAASSTEDLTNYQIGLELDNAGNVTKTKERIKAALKGEGDNNFTVSGCTEI 600  
Db 601 DGGEGRVHYSRGNYGALTIDATKETEOGSTYNRVETGKALHEVSTHTALVGNRE 660  
Qy 601 DGGEGRVHYSRGNYGALTIDATKETEOGSTYNRVETGKALHEVSTHTALVGNRE 660

RESULT 6  
ID US-08-387-156-6 STANDARD; PRT; 926 AA.  
XX  
AC xxxx  
XX  
DE Sequence 6, Application US/08387156  
CC Patent No. 5723129  
CC Sequence 6, Application US/08387156  
CC GENERAL INFORMATION:  
CC POTTIER, ANDREW A.  
CC REDMOND, MARK J.  
CC HUGHES, HOW P.A.  
CC TITLE OF INVENTION: GrRH-LEDUROTOXIN CHIMERAS  
CC NUMBER OF SEQUENCES: 28  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: REED & ROBINS  
CC STREET: 635 BRYANT STREET  
CC CITY: PALO ALTO  
CC STATE: CALIFORNIA  
CC COUNTRY: UNITED STATES OF AMERICA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: FLOPPY DISK  
CC COMPUTER: IBM PC COMPATIBLE  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/387-156  
CC FILING DATE: 10-FEB-1995  
CC CLASSIFICATION: 24  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/960, 932  
CC FILING DATE: 14-OCT-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/779, 171  
CC FILING DATE: 16-OCT-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: ROBINS, ROBERTA L.  
CC REGISTRATION NUMBER: 33,208  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 327-1231  
CC TELEFAX: (415) 617-9999  
CC INFORMATION FOR SEQ ID NO: 6:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 926 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: Linear

CC	MOLECULE TYPE:	Protein	ID:	US-07-908-253-2
SQ	SEQUENCE	926 AA; 93346 MW; 4207190 CN;	STANDARD:	PRT;
	Query Match	98.6%; Score 6128; DB 1; Length 926;		926 AA.
	Best Local Similarity	100.0%;		
	Matches	Pred. No. 0, 0.00e+00;		
	Matches	0; Mismatches 0; Indels 0; Gaps 0;		
Db	1	MATVIDLSFPKIGAKKILYIPQNYQYDTEGNGLQDLVKAEEELGIEYOREERNNTIA 60	XX	AC
Qy	1	MATVIDLSFPKIGAKKILYIPQNYQYDTEGNGLQDLVKAEEELGIEYOREERNNTIA 60	XX	xxxxxx
Db	61	QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGQALGSSEIVONANKAKTVLGSIQS 120	XX	Sequence 2, Application US/07908253
Qy	61	QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGQALGSSEIVONANKAKTVLGSIQS 120	XX	Patent No. 5534256
Db	121	IGSVLAGMDLDEALQNSNQHALAKAGLETLNSLIENIANSVKTLDFFEQISQFGSKL 180	XX	GENERAL INFORMATION:
Qy	121	IGSVLAGMDLDEALQNSNQHALAKAGLETLNSLIENIANSVKTLDFFEQISQFGSKL 180	XX	APPLICANT: POTTER, ANDREW A.
Db	181	QNTKGIGLTLGDLKNICGGLDKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 240	XX	APPLICANT: HARLAND, RICHARD J.
Qy	181	QNIKGIGLTLGDLKNICGGLDKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 240	XX	TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
Db	241	NOVGNITKAVSYILAQRVAGLSSTGPVALIYSTVSLAISPLAFLAGTADKENHAKSL 300	XX	NUMBER OF SEQUENCES: 6
Qy	241	NOVGNITKAVSYILAQRVAGLSSTGPVALIYSTVSLAISPLAFLAGTADKENHAKSL 300	XX	CORRESPONDENCE ADDRESS:
Db	301	ESYAERFKLKGVDNLIAEYQRGTGTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360	XX	CC ADDRESSEE: ROBERTA L. ROBINS
Qy	301	ESYAERFKLKGVDNLIAEYQRGTGTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360	XX	STREET: 635 BRYANT STREET
Db	361	LIVSGITGVISTILOYSKOAMEFHVANKIHNKIVEMEKNHKGKFENGDAYRLANLQD 420	XX	CITY: PALO ALTO
Qy	361	LIVSGITGVISTILOYSKOAMEFHVANKIHNKIVEMEKNHKGKFENGDAYRLANLQD 420	XX	STATE: CALIFORNIA
Db	421	NMKFLNLNKEQAEVRIATIQQQWDNNIGDLAGISRIGEKVLSKAYDAFEEGKHKA 480	XX	COUNTRY: UNITED STATES OF AMERICA
Qy	421	NMKFLNLNKEQAEVRIATIQQQWDNNIGDLAGISRIGEKVLSKAYDAFEEGKHKA 480	XX	ZIP: 941301
Db	481	DKLVQLDSANGTIDVNSNGKAKTQHILFRPLTPTEHRVQRGKYEYTAKLNIRVD 540	XX	COMPUTER READABLE FORM:
Qy	481	DKLVQLDSANGTIDVNSNGKAKTQHILFRPLTPTEHRVQRGKYEYTAKLNIRVD 540	XX	COMPUTER: IBM PC Compatible
Db	541	SWKITDGAASSFDLNVQRQGIELDNAGNVTKETKITAALKGEGDNNVFVGSGTTEI 600	XX	OPERATING SYSTEM: PC-DOS/MS-DOS
Qy	541	SWKITDGAASSFDLNVQRQGIELDNAGNVTKETKITAALKGEGDNNVFVGSGTTEI 600	XX	SOFTWARE: Patent Release #1.0, Version #1.25
Db	601	DGEGYDRHYSRGNYGALTIDATKETEIQGSYTVNRVETGKALHEVTSTHTALVNREE 660	XX	CURRENT APPLICATION DATA:
Qy	601	DGEGYDRHYSRGNYGALTIDATKETEIQGSYTVNRVETGKALHEVTSTHTALVNREE 660	XX	APPLICATION NUMBER: US/07/908, 253
Db	661	KIEYRISNNQHAGYTTKDTLKAVEELTGHSHNDIFGSKSENDAFNGDGYTDGNDGN 720	XX	FILING DATE: 19920702
Qy	661	KIEYRISNNQHAGYTTKDTLKAVEELTGHSHNDIFGSKSENDAFNGDGYTDGNDGN 720	XX	CLASSIFICATION: 420
Db	721	DRLFGGKGDDILDGGNGDDFIDGGKGNLDLHGKGDDIFVHRKGCDNDIITDSGNDKLS 780	XX	ATTORNEY/AGENT INFORMATION:
Qy	721	DRLFGGKGDDILDGGNGDDFIDGGKGNLDLHGKGDDIFVHRKGCDNDIITDSGNDKLS 780	XX	NAME: ROBINS, ROBERTA L.
Db	781	FSDSNLKDLDLTFEVKHNLYITNSKKEKVTIONWREADAKEPVNPYKATKDEKTEIIIGQ 840	XX	REGISTRATION NUMBER: 33, 208
Qy	781	FSDSNLKDLDLTFEVKHNLYITNSKKEKVTIONWREADAKEPVNPYKATKDEKTEIIIGQ 840	XX	REFERENCE/DOCKET NUMBER: 9000-0026
Db	901	DSRNVLVAPTSMLDQSLSLQFARG 926	XX	TELECOMMUNICATION INFORMATION:
Qy	901	DSRNVLVAPTSMLDQSLSLQFARG 926	XX	TELEPHONE: (415) 617-8999
Db	921	QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 986	XX	TELEFAX: (415) 327-3231
Qy	921	QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 986	XX	INFORMATION FOR SEQ ID NO: 2:
Db	981	QVYGNITKAVSSYLLAQRAAGLSSTGVAAATSYSLAISPLAFIADKENHAKSL 1050	XX	SEQUENCE CHARACTERISTICS:
Qy	981	QVYGNITKAVSSYLLAQRAAGLSSTGVAAATSYSLAISPLAFIADKENHAKSL 1050	XX	LENGTH: 926 amino acids
Db	1041	ESYAERFKLKGVDNLIAEYQRGTGTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360	XX	TYPE: AMINO ACID
Qy	1041	ESYAERFKLKGVDNLIAEYQRGTGTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360	XX	TOPOLOGY: linear
CC	SEQUENCE	926 AA; 93346 MW; 4207190 CN;	MOLECULE TYPE:	protein
SO	Query Match	98.6%; Score 6128; DB 1; Length 926;	Best Local Similarity	100.0%; Pred. No. 0, 0.00e+00;
	Matches	926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	1	MATVIDLSFPKIGAKKILYIPQNYQYDTEGNGLQDLVKAEEELGIEYOREERNNTIA 60	Db	1 MATVIDLSFPKIGAKKILYIPQNYQYDTEGNGLQDLVKAEEELGIEYOREERNNTIA 60
Qy	1	QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 986	Qy	1 MATVIDLSFPKIGAKKILYIPQNYQYDTEGNGLQDLVKAEEELGIEYOREERNNTIA 60
Db	61	QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 986	Db	61 QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 986
Qy	61	QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 986	Qy	61 QTSLGQTQTAIGLTERTIVLSPAQIDKLQKTKAGLGLDVISGLSGATAALVLADKNASTAKKVGAGFELA 986
Db	121	LGSVLAGMDLDEALQNSNQHALAKAGLETLNSLIENIANSVKTLDFFEQISQFGSKL 180	Db	121 LGSVLAGMDLDEALQNSNQHALAKAGLETLNSLIENIANSVKTLDFFEQISQFGSKL 180
Qy	121	LGSVLAGMDLDEALQNSNQHALAKAGLETLNSLIENIANSVKTLDFFEQISQFGSKL 180	Qy	121 LGSVLAGMDLDEALQNSNQHALAKAGLETLNSLIENIANSVKTLDFFEQISQFGSKL 180
Db	181	QVYGNITKAVSSYLLAQRAAGLSSTGVAAATSYSLAISPLAFIADKENHAKSL 300	Db	181 QVYGNITKAVSSYLLAQRAAGLSSTGVAAATSYSLAISPLAFIADKENHAKSL 300
Qy	181	QVYGNITKAVSSYLLAQRAAGLSSTGVAAATSYSLAISPLAFIADKENHAKSL 300	Qy	181 QVYGNITKAVSSYLLAQRAAGLSSTGVAAATSYSLAISPLAFIADKENHAKSL 300
Db	301	ESYAERFKLKGVDNLIAEYQRGTGTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360	Db	301 ESYAERFKLKGVDNLIAEYQRGTGTIDASVTAINTALAAIAGGVSAAAGSVIASPIA 360
RESULT	7			

301 ESYAERFKKKLGNDNLIAEYORGTTIDASVTAINTALAAJAGYSAAAAGSVIASPIA 360  
 361 LIVSGITGVISTLQYSKQAMFEHVANKHNKIVEWKNNHKGKNYFENGDARYLANQD 420  
 361 LIVSGITGVISTLQYSKQAMFEHVANKHNKIVEWKNNHKGKNYFENGDARYLANQD 420  
 421 NMKFLLNNEKEQAERYTAITQQWDNNIGDLAGISRGEKYLGSRAYVDAEEGHKHA 480  
 421 NMKFLLNNEKEQAERYTAITQQWDNNIGDLAGISRGEKYLGSRAYVDAEEGHKHA 480  
 QY 481 DLVLOLDANG1DVNSNGKATQHILFRTPGTEHREVQTYGRKEYTTLKNINRVD 540  
 QY 481 DLVLOLDANG1DVNSNGKATQHILFRTPGTEHREVQTYGRKEYTTLKNINRVD 540  
 DB 541 SWKTDGASSSTEDLNVRQIGIELDNGNNTKTKTIIAKLGDDDNFVGSGTTEI 600  
 QY 541 SWKTDGASSSTEDLNVRQIGIELDNGNNTKTKTIIAKLGDDDNFVGSGTTEI 600  
 DB 601 DGGEGDVRHYSSGNYGAUTIDATEKEPQGSTVNRPETGALHEVTSTHTALYGNREE 660  
 QY 601 DGGEGDVRHYSSGNYGAUTIDATEKEPQGSTVNRPETGALHEVTSTHTALYGNREE 660  
 DB 661 KIEYRHSNNOHAGYTTKDTLKAVEETIGTSNDIFGSKFENDAFNGDGYDTIDGNDGN 720  
 QY 661 KIEYRHSNNOHAGYTTKDTLKAVEETIGTSNDIFGSKFENDAFNGDGYDTIDGNDGN 720  
 DB 721 DRFLGGKDDIDLGCGNDFDEIDCGKGNDLILAGGKDDIFVHRKGNDNIDITSDGNDKL 780  
 QY 721 DRFLGGKDDIDLGCGNDFDEIDCGKGNDLILAGGKDDIFVHRKGNDNIDITSDGNDKL 780  
 DB 781 FDSGNLKDITFEVKHNVITNSKKEVTIONWREADFAKEPVNYKATKDKSIEETIGO 840  
 QY 781 FDSGNLKDITFEVKHNVITNSKKEVTIONWREADFAKEPVNYKATKDKSIEETIGO 840  
 DB 841 NGERITSKQVDLIAKNGKKITODELSKVVDYELKHKSNTVNSLDKLISSVSAFTSSN 900  
 QY 841 NGERITSKQVDLIAKNGKKITODELSKVVDYELKHKSNTVNSLDKLISSVSAFTSSN 900  
 DB 901 DSRYVLVAPTSMLDQSSLQFARGS 926  
 QY 901 DSRYVLVAPTSMLDQSSLQFARGS 926

RESULT 8  
 ID US-08-455-970A-2 STANDARD; PRT; 926 AA.  
 XX xxxxxx  
 AC  
 XX  
 DT  
 XX  
 DE Sequence 2, Application US/08455970A  
 Sequence 2, Application US/08455970A  
 Patent No. 5708155  
 GENERAL INFORMATION:  
 APPLICANT: POTTER, ANDREW A.  
 APPLICANT: REDMOND, MARK J.  
 APPLICANT: HUGHES, HOW P.A.  
 TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
 TITLE OF INVENTION: CHIMERAS  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: REED & ROBINS  
 STREET: 285 HAMILTON AVENUE, SUITE 200  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455-970A  
 FILING DATE: 31-MAY-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/960, 932  
 FILING DATE: 14-OCT-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ROBINS, ROBERT L.  
 REGISTRATION NUMBER: 33-208  
 REFERENCE/DOCKET NUMBER: 9001-0016-10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 327-3400  
 TELEFAX: (415) 327-3231  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 926 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 CC SEQUENCE 926 AA; 9934 MW; 4207190 CN;  
 CC Query Match 98.6%; Score 6128; DB 1; Length 926;  
 CC Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 CC Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 MATVIDISSEPTGAKKILIPQNYQYDTEQNGLQDLYKRAAEELGIVREERNNIATA 60  
 QY 1 MATVIDISSEPTGAKKILIPQNYQYDTEQNGLQDLYKRAAEELGIVREERNNIATA 60  
 Db 61 QTSLGTTQTAIGLTERGVILSAPQIDKLQTKAGQALGSAESTYQANAKTAKVTLGQS 120  
 QY 61 QTSLGTTQTAIGLTERGVILSAPQIDKLQTKAGQALGSAESTYQANAKTAKVTLGQS 120  
 DB 121 LGSVLAGMDDEALNNNSNOHALAKAGELTNSLIENTANSVKTDEFQEIQISFGSKL 180  
 QY 121 QNIKGIGLTGDKLKNIGGLDRAGLGLDVISSLSGATAVLYLADKNASTAKVGAFFELA 180  
 DB 1241 NOVVGNTKAVSSYLLAQDRVAGLSSTGPYALIATSVLAIISPLAFAGTADKENFAKSL 300  
 QY 1241 NOVVGNTKAVSSYLLAQDRVAGLSSTGPYALIATSVLAIISPLAFAGTADKENFAKSL 300  
 DB 301 ESYAERFKLKGQYDGDNLIAEYORGTTIDASVTAINTALAAJAGYSAAAAGSVIASPIA 360  
 QY 301 ESYAERFKLKGQYDGDNLIAEYORGTTIDASVTAINTALAAJAGYSAAAAGSVIASPIA 360  
 DB 421 NMKFLNLINKELQQAERYTAITQOQNINIDQIAGTSRGEKVLGKAYDAFEEGHKHA 480  
 QY 421 NMKFLNLINKELQQAERYTAITQOQNINIDQIAGTSRGEKVLGKAYDAFEEGHKHA 480  
 DB 361 LLVSGITGVISTLQYSKQAMFEHVANKHNKIVEWKNNHKGKNYFENGDARYLANQD 420  
 QY 361 LLVSGITGVISTLQYSKQAMFEHVANKHNKIVEWKNNHKGKNYFENGDARYLANQD 420  
 DB 481 DLVQLDANG1DVNSGKATQHILFRTPGTEHREVQTYGRKEYTTLKNINRVD 540  
 QY 481 DLVQLDANG1DVNSGKATQHILFRTPGTEHREVQTYGRKEYTTLKNINRVD 540  
 DB 541 SWKTDGASSSTEDLNVRQIGIELDNGNNTKTKTIIAKLGDDDNFVGSGTTEI 600  
 QY 541 SWKTDGASSSTEDLNVRQIGIELDNGNNTKTKTIIAKLGDDDNFVGSGTTEI 600  
 DB 601 DGEGYDVRHVSRGNYGALTIDATEKEPQGSTVNRPETGALHEVTSTHTALYGNREE 660  
 QY 601 DGEGYDVRHVSRGNYGALTIDATEKEPQGSTVNRPETGALHEVTSTHTALYGNREE 660  
 DB 661 KIEYRHSNNOHAGYTTKDTLKAVEETIGTSNDIFGSKFNDAFGDGYDTIDGNDGN 720  
 QY 661 KIEYRHSNNOHAGYTTKDTLKAVEETIGTSNDIFGSKFNDAFGDGYDTIDGNDGN 720

RESULT 9  
 ID US-08-455-970-A0 STANDARD; PRT; 943 AA.  
 XX xxxxxx  
 XX  
 DE Sequence 10, Application US/08455970A  
 XX  
 Sequence 10, Application US/08455970A  
 CC Patent No. 5708155  
 CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC APPLICANT: REDMOND, MARK J.  
 CC APPLICANT: HUGHES, HOW P. A.  
 CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
 CC NUMBER OF SEQUENCES: 15  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: REED & ROBINS  
 STREET: 285 HAMILTON AVENUE, SUITE 200  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 94301  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: FLOPPY disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/455, 970A  
 CC FILING DATE: 31-MAY-1995  
 CC CLASSIFICATION: 424  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/960, 932  
 CC FILING DATE: 14-OCT-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: ROBINS, ROBERTA L.  
 CC REGISTRATION NUMBER: 33,208  
 CC REFERENCE/DOCKET NUMBER: 9001-0016.10  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 327-3400  
 CC TELEFAX: (415) 327-3231  
 CC INFORMATION FOR SEQ ID NO: 10:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 943 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: Protein  
 SQ SEQUENCE 943 AA; 101229 MW; 4397993 CN;

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Db 721 DRLEFGGKGGDDILDGGNGDDFDIGGKGNDLLHGKGDDIFVHRKGNDLITDSGNDKL 780  
 Qy 721 DRLEFGGKGGDDILDGGNGDDFDIGGKGNDLLHGKGDDIFVHRKGNDLITDSGNDKL 780  
 Db 781 FDSNKLKDLEFEVKHNLTINSKKEKTYONWREADFAKEPVNYKATKDEKEETIGQ 840  
 Qy 781 FDSNKLKDLEFEVKHNLTINSKKEKTYONWREADFAKEPVNYKATKDEKEETIGQ 840  
 Db 841 NGERITSKQVDDLIAKNGKTTQDELSKVVDYELLKHSKNVTNSLDKLISSVSAFTSSN 900  
 Qy 841 NGERITSKQVDDLIAKNGKTTQDELSKVVDYELLKHSKNVTNSLDKLISSVSAFTSSN 900  
 Db 901 DSRNVLVAPTSMDQSLSSLOFARG 926  
 Qy 901 DSRNVLVAPTSMDQSLSSLOFARG 926

Db 1 MATVIDLSSPPTGAKKKILLYIPONYQYDTEQNGLQDLVKAABELGIEVQREERNNTATA 60  
 Qy 1 MATVIDLSSPPTGAKKKILLYIPONYQYDTEQNGLQDLVKAABELGIEVQREERNNTATA 60  
 Db 61 QTSELGTTQAGTGTBERGIVTLSAPOIDKLQKTRAGQALGSAESTIVQNANKAKTVLSGIQ 120  
 Qy 61 QTSELGTTQAGTGTBERGIVTLSAPOIDKLQKTRAGQALGSAESTIVQNANKAKTVLSGIQ 120  
 Db 121 ILGSVLAGMDLDEALQNNSNQHALAKAGELTNSLIENIANSVKTLDGEQISQFGSKL 180  
 Qy 121 ILGSVLAGMDLDEALQNNSNQHALAKAGELTNSLIENIANSVKTLDGEQISQFGSKL 180  
 Db 181 QNIKGLTGDKLKKNIGGDKAGLGLDVSGLSGATAVLADKNASTAKVYGAFFLA 240  
 Qy 181 QNIKGLTGDKLKKNIGGDKAGLGLDVSGLSGATAVLADKNASTAKVYGAFFLA 240  
 Db 241 NOVGNNTPAVSSYLAQRYAAGLJSSTGEVAJLIASTYSLAISPLAFAGIADKFNHAKSL 300  
 Qy 241 NOVGNNTPAVSSYLAQRYAAGLJSSTGEVAJLIASTYSLAISPLAFAGIADKFNHAKSL 300  
 Db 301 ESYAERFKLKGYGDNLIAEYORGTTGTDASVTAINTALAATAGGVSAAAGSVIASPIA 360  
 DT 301 ESYAERFKLKGYGDNLIAEYORGTTGTDASVTAINTALAATAGGVSAAAGSVIASPIA 360  
 Db 361 LLYSGITGWISTLQLQSKQAMFHVANKLNKIVWEKNHGNKYFENGVDARYLANLQD 420  
 Qy 361 LLYSGITGWISTLQLQSKQAMFHVANKLNKIVWEKNHGNKYFENGVDARYLANLQD 420  
 Db 421 NMKEFLNNKELQAVERTIAITQQWDNNJNQDLAGISRLGKAVYDAFBEGKHKIA 480  
 Qy 421 NMKEFLNNKELQAVERTIAITQQWDNNJNQDLAGISRLGKAVYDAFBEGKHKIA 480  
 Db 481 DKLYQLDSANGLIDVNSGAKTOHILFRPLTPGTEHREVQTYKYEITKLNINRVD 540  
 Qy 481 DKLYQLDSANGLIDVNSGAKTOHILFRPLTPGTEHREVQTYKYEITKLNINRVD 540  
 Db 541 SWKTDGAASSTFDTLNVYQRTGELDNAGNTKTKTIIAKLGEDDDNFVGSGNTEI 600  
 Qy 541 SWKTDGAASSTFDTLNVYQRTGELDNAGNTKTKTIIAKLGEDDDNFVGSGNTEI 600  
 Db 601 DGGBGYDRWHYSGRNQGALTIATKETEQGSTVNRFETGVALHEVSTHFLVGARE 660  
 Qy 601 DGGBGYDRWHYSGRNQGALTIATKETEQGSTVNRFETGVALHEVSTHFLVGARE 660  
 Db 721 DRLEFGGKGDDILDGGNGDDFDIGGKGNDLIIITSDGNDKL 780  
 Qy 721 DRLEFGGKGDDILDGGNGDDFDIGGKGNDLIIITSDGNDKL 780  
 Db 781 FDSNLKDLEFEVKHNLTINSKKEVYIOWFREADFAKEPVNYKATKDEKEETIGQ 840  
 Qy 781 FDSNLKDLEFEVKHNLTINSKKEVYIOWFREADFAKEPVNYKATKDEKEETIGQ 840  
 Db 841 NGERITSKQVDDLIAKNGKTTQDELSKVVDYELLKHSKNVTNSLDKLISSVSAFTSSN 900  
 Qy 841 NGERITSKQVDDLIAKNGKTTQDELSKVVDYELLKHSKNVTNSLDKLISSVSAFTSSN 900  
 Db 901 DSRNVLYAPTSMDQSLSSLOFARG 926  
 Qy 901 DSRNVLYAPTSMDQSLSSLOFARG 926

RESULT 10  
 ID US-08-455-970-A14 STANDARD;  
 XX  
 AC  
 XX  
 DT  
 XX  
 XX

xxxxxx

xxxxxx

xx

Query Match 98.6%; Score 6128; DB 1; Length 943;

Best Local Similarity 100.0%; Pred. No. 0.00e+00; Indels 0; Gaps 0;

Matches 926; Conservative

DE Sequence 14 , Application US/08455970A  
 XX Sequence 14 , Application US/08455970A  
 CC Patent No. 5708155  
 CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC APPLICANT: REDMOND, MARK J.  
 CC APPLICANT: HUGHES, HUN P.A.  
 CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
 CC NUMBER OF SEQUENCES: 15  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSE: REED & ROBINS  
 CC STREET: 285 HAMILTON AVENUE, SUITE 200  
 CC CITY: PALO ALTO  
 CC STATE: CALIFORNIA  
 CC COUNTRY: UNITED STATES OF AMERICA  
 CC ZIP: 94301  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/455, 970A  
 CC FILING DATE: 31-MAY-1995  
 CC CLASSIFICATION: 424  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/960, 932  
 CC FILING DATE: 14-OCT-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: ROBINS, ROBERTA L.  
 CC REGISTRATION NUMBER: 33,208  
 CC REFERENCE/DOCKET NUMBER: 9001-0016-10  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 327-3400  
 CC TELEFAX: (415) 327-3231  
 CC INFORMATION FOR SEQ ID NO: 14:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 951 amino acids  
 CC TOPOLGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 951 AA: 102128 MW: 4463354 CN:  
 SQ Query Match 98.5%; Score 6128; DB 1; Length 951;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	MATYDLSFPKTAGKKLILYIPQNYQDTEQGNGLDLYKAELGIEVQREERNNTATA	60
Qy	1	MATYDLSFPKTAGKKLILYIPQNYQDTEQGNGLDLYKAELGIEVQREERNNTATA	60
Db	61	QTSLGTIQTAIGLTERGIVLsapQDQLKLQKTKAGQALGSAESTVNANKATVLSGQS	120
Qy	61	QTSLGTIQTAIGLTERGIVLsapQDQLKLQKTKAGQALGSAESTVNANKATVLSGQS	120
Db	121	LGGSVLAGMDLEALQNNSNQHALAKAGLELTNSLIENANSYKTLDFEGIQSOFGSKL	180
Qy	121	LGGSVLAGMDLEALQNNSNQHALAKAGLELTNSLIENANSYKTLDFEGIQSOFGSKL	180
Db	181	QNIKGLGTIDGKLNIGGLDLAGLDTGQIISQFGSKL	240
Qy	181	QNIKGLGTIDGKLNIGGLDLAGLDTGQIISQFGSKL	240
Db	241	NOVYGNITKAVSSYLAQRVAGLSSTGPVALIATYSTSIAISPLAFAGIADKFNHAKSL	300
Qy	241	NOVYGNITKAVSSYLAQRVAGLSSTGPVALIATYSTSIAISPLAFAGIADKFNHAKSL	300
Db	301	ESYAERFKKLQGYDGNLIALEYQRTGTIDASVTAINTALAAIAGVSAAAGSVIASPIA	360
Qy	301	ESYAERFKKLQGYDGNLIALEYQRTGTIDASVTAINTALAAIAGVSAAAGSVIASPIA	360

SQ RESULT 11  
 ID US-08-170-126-2 STANDARD;  
 XX PRT; 1098 AA.  
 AC XXXXX

Sequence 2, Application US/08170126  
 CC Sequence 2, Application US/08170126  
 CC Patent No. 5594107  
 CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW  
 CC APPLICANT: CAMPOS, MANUEL  
 CC APPLICANT: HUGHES, HUN P.A.  
 CC TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES  
 CC NUMBER OF SEQUENCES: 6  
 CC TITLE OF INVENTION: CYTOKINE  
 CC NUMBER OF SEQUENCES: 6  
 CC CORRESPONDENCE ADDRESS:  
 CC STREET: 635 BRYANT STREET  
 CC CITY: PALO ALTO  
 CC STATE: CALIFORNIA  
 CC COUNTRY: UNITED STATES OF AMERICA  
 CC ZIP: 94301  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/170-126

CC	FILING DATE: 20-DEC-1993	Db	903	ILDGNGDFTDGGKGNDLHGGDDITVHRKGNDLITDSDGNDKLSFSDSNLKDLT 962
CC	CLASSIFICATION: 530	Qy	731	ILDGNGDFTDGGKGNDLHGGDDITVHRKGNDLITDSDGNDKLSFSDSNLKDLT 790
CC	PRIOR APPLICATION DATA:	US 07/777,715	Db	963 FEKYKHNLTNSKEKVYTKVQNWFREADAKEPVNYKATKDEKEEIQNGERITSKQV 1022
CC	APPLICATION NUMBER:	US 07/571,301	Qy	791 FEKYKHNLTNSKEKVYTKVQNWFREADAKEPVNYKATKDEKEEIQNGERITSKQV 850
CC	ATTORNEY/AGENT INFORMATION:		Db	1023 DDLIAKGNGKITDLSKVVDLYELLKHSKVINSLDKLISSYAFTSSNDSRNVLVAPT 1082
CC	NAME: ROBINS, ROBERTA L.		Qy	851 DDLIAKGNGKITDLSKVVDLYELLKHSKVINSLDKLISSYAFTSSNDSRNVLVAPT 910
CC	REGISTRATION NUMBER: 33,208	Db	1083 SMLDOSLSLSQLFARS 1098	
CC	REFERENCE/DOCKET NUMBER: 9000-0013-21	Qy	911 SMLDOSLSLSQLFARS 926	
CC	TELECOMMUNICATION INFORMATION:		RESULT 12	
CC	TELEPHONE: (415) 327-3231	ID	US-07-777-715-7	
CC	TELEFAX: (415) 617-8999	STANDARD;		
CC	INFORMATION FOR SEQ ID NO: 2:	XX	PRT;	
CC	SEQUENCE CHARACTERISTICS:	AC	1098 AA.	
CC	LENGTH: 1098 amino acids	xxxxxx		
CC	TYPE: amino acid			
CC	TOPOLOGY: linear			
CC	MOLECULE TYPE: protein			
SQ	SEQUENCE 1098 AA: 118577 MW: 5903750 CN;			
	Query Match Score 97.4%; Best Local Similarity 100.0%;	XX		
	Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX		
Db	183 KTGAKKILYIPQNYQYDTEQGNGLQDLVRAEELGIEYERERNNTIATQSLOTIQA 242	XX	Sequence 7, Application US/07777715	
Qy	11 KTGAKKILYIPQNYQYDTEQGNGLQDLVRAEELGIEYERERNNTIATQSLOTIQA 70	XX	Sequence 7, Application US/07777715	
Db	243 IGLTERGIVLSPAPQIDKLQKTAGQALGSAEVYONANKAKTVLGSIQSLSGYLAGMD 302	XX	Patent No. 5273889	
Qy	71 IGLTERGIVLSPAPQIDKLQKTAGQALGSAEVYONANKAKTVLGSIQSLSGYLAGMD 130	XX	GENERAL INFORMATION:	
Db	303 LEBALQNSNQHALAKAGLETNSLIENTANSVKTIDFEQEISQFGSKLQNKIGLGTLG 362	XX	APPLICANT: Potter, Andrew	
Qy	131 LEBALQNSNQHALAKAGLETNSLIENTANSVKTIDFEQEISQFGSKLQNKIGLGTLG 190	XX	APPLICANT: Campos, Manuel	
Db	363 DKLKNIGLGLDKAGLGLDVISGLSGATAALYLAQDNASTARKVAGFELANQVGNITKA 422	XX	APPLICANT: Hughes, Huw P.A.	
Qy	191 DKLKNIGLGLDKAGLGLDVISGLSGATAALVADKNASTARKVAGFELANQVGNITKA 250	XX	TITLE OF INVENTION: CYTOKINE LEUKOTOXIN GENE FUSIONS AND	
Db	423 VSSYILAQRVAAGLSSSTGPVALIATSVLAIPLAFAGIADKENHAKSLEYAERFKL 482	XX	USES THEREOF	
Qy	251 VSSYILAQRVAAGLSSSTGPVALIATSVLAIPLAFAGIADKENHAKSLEYAERFKL 310	XX	NUMBER OF SEQUENCES: 9	
Db	483 GVDGDNLAAEYORGTTIDASVTAINTALAAGGYSAAAGSVIASPIALVSGITVI 542	XX	CORRESPONDENCE ADDRESS:	
Qy	311 GVDGDNLAAEYORGTTIDASVTAINTALAAGGYSAAAGSVIASPIALVSGITVI 370	XX	ADDRESSEE: Morrison & Foerster	
Db	543 STILOYSKQAMEHEVANKIHNKIVENNGKNTFENGDAYRLANLQDNMKFLNLNK 602	XX	STREET: 545 Middlefield Road, Suite 200	
Qy	371 STILOYSKQAMEHEVANKIHNKIVENNGKNTFENGDAYRLANLQDNMKFLNLNK 430	XX	CITY: Menlo Park	
Db	603 ELOAERVIATQQQWNNGNIDAGISRLGERKVLGSKAYDAFEEGHKIKADLYVOLDSAN 662	XX	STATE: California	
Qy	431 ELOAERVIATQQQWNNGNIDAGISRLGERKVLGSKAYDAFEEGHKIKADLYVOLDSAN 490	XX	COUNTRY: USA	
Db	663 GLIDVNSNGKAKTQHILFRPLTPGEHREVQTKYETKLNTRDWSKTKDGAAS 722	XX	ZIP: 94025	
Qy	491 GLIDVNSNGKAKTQHILFRPLTPGEHREVQTKYETKLNTRDWSKTKDGAAS 550	XX	COMPUTER READABLE FORM:	
Db	723 STFDLTNVQRGFIELDNAGNYKTRETKEALKLGEGDDNVFGSGTEIDGEGYDRVH 782	XX	MEDIUM TYPE: Floppy disk	
Qy	551 STFDLTNVQRGFIELDNAGNYKTRETKEALKLGEGDDNVFGSGTEIDGEGYDRVH 710	XX	COMPUTER: IBM PC Compatible	
Db	783 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALYGNREEKTYRHNNQ 842	XX	OPERATING SYSTEM: PC-DOS/MS-DOS	
Qy	611 YSRGNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALYGNREEKTYRHNNQ 670	XX	SOFTWARE: Patentin Release #1.0, version #1.25	
Db	843 HAGYXTKDLSKAKVEETIGTSNDIIFGSKSNDIADFNGDGYDTIDNGDNRFLFGKKQD 902	XX	CURRENT APPLICATION DATA:	
Qy	671 HAGYXTKDLSKAKVEETIGTSNDIIFGSKSNDIADFNGDGYDTIDNGDNRFLFGKKQD 730	XX	APPLICATION NUMBER: US/07/777,715	
	Query Match Score 97.4%; Best Local Similarity 100.0%;	CC	FILING DATE: 1991/01/16	
	Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	ATTORNEY/AGENT INFORMATION:	
	SEQUENCE CHARACTERISTICS:	CC	NAME: Robins, Roberta L.	
	LENGTH: 1098 amino acids	CC	REGISTRATION NUMBER: 33,208	
	TYPE: AMINO ACID	CC	REFERENCE DOCKET NUMBER: 29310-2001340	
	TOPOLOGY: linear	CC	TELECOMMUNICATION INFORMATION:	
	MOLECULE TYPE: Protein	CC	TELEPHONE: 415-327-2950	
	SEQUENCE 1098 AA: 118577 MW: 5903750 CN;	CC	TELEFAX: 415-327-2951	
Db	183 KTGAKKILYIPQNYQYDTEQGNGKNTFENGDAYRLANLQDNMKFLNLNK 242	Db	INFORMATION FOR SEQ ID NO: 7:	

Qy 11 KTGAKKILILYIPQNYOYDTECGINGLGLVKAAEELGIEYQREERNIATATSLGTTIQT A 70  
 Db 243 IGLTERCIVLSPAPQIKLQLQTKAGQALGSSESTVQANAKTFVLSIQISLGSLAGMD 302  
 Qy 71 IGLTERCIVLSPAPQIKLQLQTKAGQALGSSESTVQANAKTFVLSIQISLGSLAGMD 130  
 Db 303 LDEALQNNSNQHALAKAGLELTNSLENIANSVKTLDDEFEQIOSFGSKLQNQKIGLTLG 362  
 Qy 131 LDEALQNNSNQHALAKAGLELTNSLENIANSVKTLDDEFEQIOSFGSKLQNQKIGLTLG 190  
 Db 363 DRLKNIGGLDLAGLGLDVISGLSGATAALYLADKNASTARKVAGFELANQYVGNNTKA 422  
 Qy 191 DRLKNIGGLDLAGLGLDVISGLSGATAALYLADKNASTARKVAGFELANQYVGNNTKA 250  
 Db 423 VSSYLAQRVAGLSSGPVANLIATSVLAPSPLAFAGIADKPNHAKSLESYAERFKKL 482  
 Qy 251 VSSYLAQRVAGLSSGPVANLIATSVLAPSPLAFAGIADKPNHAKSLESYAERFKKL 310  
 Db 483 GYDGDNILAEYORGTTGTIDASVTAINTALAAATAGGVSAAAGSVIASPIALLVSGITGV 542  
 Qy 311 GYDGDNILAEYORGTTGTIDASVTAINTALAAATAGGVSAAAGSVIASPIALLVSGITGV 370  
 Db 543 STILOYSKQAMFEHVANKIHNNKIVENKEKNNGKNTFENGTDARYLANLQDNMKFLINLNK 602  
 Qy 371 STILOYSKQAMFEHVANKIHNNKIVENKEKNNGKNTFENGTDARYLANLQDNMKFLINLNK 430  
 Db 603 EOQERVIAITCQODNNIGDLAGISRLGEKVLSGRAYDAFEEGHKHAKDLYVQOLDSDN 662  
 Qy 431 EOQERVIAITCQODNNIGDLAGISRLGEKVLSGRAYDAFEEGHKHAKDLYVQOLDSDN 490  
 Db 663 GIDVNSNSGRKARTQHILFRTPLLPTGEHRVOTKRYETIKLNLNRVDWSWKTIDGAAS 722  
 Qy 491 GIDVNSNSGRKARTQHILFRTPLLPTGEHRVOTKRYETIKLNLNRVDWSWKTIDGAAS 550  
 Db 723 SFDLTNVYORIGIELDNGAHTKTKETKIIAKLGEKVLSGRAYDAFEEGSYDRVH 782  
 Qy 551 SFDLTNVYORIGIELDNGAHTKTKETKIIAKLGEKVLSGRAYDAFEEGSYDRVH 610  
 Db 783 YSRGNYGALTIDATKETEQGSTVNRFVETKALHEVTSHTALVNREEKEYRHSSNQ 842  
 Qy 611 YSRGNYGALTIDATKETEQGSTVNRFVETKALHEVTSHTALVNREEKEYRHSSNQ 670  
 Db 843 HHAGYTTKDTLKAVEETIGTSINDIFPGSKFKNDFAFNGDGYTIDGNDGNPLFGKGDD 902  
 Sq 671 HHAGYTTKDTLKAVEETIGTSINDIFPGSKFKNDFAFNGDGYTIDGNDGNPLFGKGDD 730  
 Db 903 ILDGNGDDFTIGGKGNDLHLHGKGDDFTIVHRKGNDLHTDSGDGNDKLSPDSNFKDLT 962  
 Qy 731 ILDGNGDDFTIGGKGNDLHLHGKGDDFTIVHRKGNDLHTDSGDGNDKLSPDSNFKDLT 790  
 Db 963 FERVKHNLVITNSKKEKVTONFWREADFKEVPKNATKDEKIEELIGQNGERTSKV 1022  
 Qy 791 FERVKHNLVITNSKKEKVTONFWREADFKEVPKNATKDEKIEELIGQNGERTSKV 850  
 Db 1023 DDLJAKNGKTKTQDELSRKYDVEELKHSKNTNSLDKLISSSVAFSSNDRNVLVAPT 1082  
 Qy 851 DDLJAKNGKTKTQDELSRKYDVEELKHSKNTNSLDKLISSSVAFSSNDRNVLVAPT 910  
 Db 1083 SMDQSLSSLQFARG 1098  
 Qy 911 SMDQSLSSLQFARG 926

RESULT 13  
 ID US-08-215-805A-80 STANDARD PRT: 934 AA.  
 XX  
 AC  
 XX  
 DT  
 XX  
 DE  
 XX  
 CC

Patent No. 5559008  
 GENERAL INFORMATION:  
 APPLICANT: Chang, Yung-Fu  
 TITLE OF INVENTION: LEUROTOXIN GENE FROM PASTEURELLA  
 TITLE OF INVENTION: suis  
 NUMBER OF SEQUENCES: 84  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
 STREET: Clinton Square, P.O. Box 1051  
 CITY: Rochester  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 14603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/215,805A  
 FILING DATE: 22-MAR-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Timian, Susan J.  
 REGISTRATION NUMBER: 34,103  
 REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (716) 263-1636  
 TELEFAX: (716) 263-1600  
 INFORMATION FOR SEQ ID NO: 80:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 934 amino acids  
 STRANDEDNESS:  
 TOPOLogy: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Pasteurella suis  
 STRAIN: 5943  
 IMMEDIATE SOURCE:  
 LIBRARY: P. suis DNA in Bacteriophage lambda-dash  
 CLONE: (Lambda)Yfr53-37  
 SEQUENCE: 934 AA; 100477 MW; 4245576 CN;

Query Match 79.28; Score: 4925; DB 1; Length: 934;  
 Best Local Similarity 79.3%; Pred. No. 0.00e+00;  
 Matches 705; Conservative 112; Mismatches 66; Indels 1; Gaps 1;

Db 34 KAGAKKLITYIPKDYEDSGRGNGLQDLYKAEDLGIEYQREERNGIATAQNSLSTIONI 93  
 Qy 11 KTGAKKLITYIPQNYDQNGQDLYKAEEELGIEYQREERNGIATAQNSLSTIONI 70  
 Db 94 LGFSERGVVLSPAPQDLKLQYKISKAPGSESENAYKLNQNAOTLGSQISLGSMAGMD 153  
 Qy 71 IGLTERGTVLSPAPQDLKLQYKQALGSAESITVQANAKRATVLSQISLGSMAGMD 130  
 Db 154 DKLKNFGSFSKAGLGELEVIGLSSGATAALVLDKNASTDRKGAGFELANQYVGNNTKA 273  
 Qy 131 LDEALQNNSNQHALAKGELTNTSLIENTANSVKTLDGEQISOGSKLQNLIGLTLG 190  
 Db 214 DKLKNFGSFSKAGLGELEVIGLSSGATAALVLDKNASTDRKGAGFELANQYVGNNTKA 273  
 Qy 191 DRLKNIGGLDLAGLGLDVISGLSSATAALVLDENASTAKVAGFELANQYVGNNTKA 250  
 Db 274 VSSYLAQRYAAGLSSNTGPVSLAISTVALAISPLAFAGIADKENAKALESYAERFKKL 333  
 Qy 251 VSSYLAQRYAAGLSSNTGPVAAIATSVSISPLAFAGIADKENAKALESYAERFKKL 310  
 Db 334 GYEGDSLAEYORGTTGIDASVTANTALAIAGGSAAGSLVYVAPALLYSITGII 393  
 Qy 311 GYDGDNILAEYORGTTGIDASVTANTALAIAGGSAAGSLVYVAPALLYSITGII 370  
 Db 394 STILOYSKQAMFEHVANKIHDKIVDWEKHHNGKNTFENGDSRYLADQDNMROLQNLK 453

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 371 STILOYSKQMFHEVANKLNKIVEWENHGGNKFENYDARYLANLQDNMFLNLNK 430  
 Qy CC REFERENCE/DOCKET NUMBER: 19603/00001  
 Db CC TELECOMMUNICATION INFORMATION:  
 Db CC TELEPHONE: 716-853-8104  
 Db CC TELEFAX: 716-853-8109  
 Qy CC INFORMATION FOR SEQ ID NO: 2:  
 Db CC SEQUENCE CHARACTERISTICS:  
 Db CC LENGTH: 1244 amino acids  
 Db CC TYPE: amino acid  
 Db CC STRANDEDNESS: double  
 Db CC TOPOLOGY: linear  
 Db CC MOLECULE TYPE: peptide  
 Qy CC HYPOTHETICAL: NO  
 Db CC FRAGMENT TYPE: N-terminal  
 Db CC ORIGINAL SOURCE:  
 Db CC ORGANISM: *Actinobacillus pleuropneumoniae*  
 Db CC STRAIN: Serotypes 2, 3, 4, 6 and 8  
 Db CC INDIVIDUAL ISOLATE: Swine  
 Db CC CELL TYPE: Gram negative bacterium  
 Qy CC SEQUENCE: 1244 AA; 135397 MW; 7631235 CN;  
 Query Match 41.3%; Score: 2566; DB: 2; Length: 1244;  
 Best Local Similarity 52.2%; Pred. No. 6.12e-18;  
 Matches 401; Conservative 177; Mismatches 167; Indels 23; Gaps 20;  
 Db 228 GNKLVLVIP-K EYDGSVNGEFDLYKAEEELGIQKYVNNNELEYAKSLGTADOFGLI 285  
 Qy 14 AKKILYTPQNTQYDTEQQGLQDLKAAEELGIEQREERNNTIAATQSLGTQTAIGL 73  
 Db 286 TERGLTLPAPQLDQFLQKHSKLESNVGSSGTGDAVSKLAKSQTISQISVLTLAGINL 345  
 Qy ||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 74 TERGVILSAPQDKLQLQ-TKAGQALGSAES-TQVNANKAKTVLSLQISLGSVLAGMDL 131  
 Qy 74 NEAIISSGESELEAEGVSASLSELVNTAIKGTTIDAFTOIQTNQFG-KLAENAKGLGGVG 404  
 Db 132 DEALQNNNSQHALAKAGLETLSLIERANSYTKLDEFGQISQFSSKL-ONIKGIGTLG 190  
 Qy 405 RQQNISGSALSSTKTGGLDIDISLLSGTSVTRSPALRNKNASTSTKVAAFGESNQVIGGIT 464  
 Db 191 DLKRNIGG-LDKAGLGDIVTGLLSSATTAIALYLDKNASTAKKVAEGELANQVGNIT 248  
 Db 465 KAVSSYLLAQRLRAGLSTTGPAAALTISIISPLAFLRYADNFNSKEIGEFAERFK 524  
 Qy 309 KLGYGDNLIAEYQRTGTTGDSVTAINTALAATAGVSAAAGSVTASPALLYSGITG 368  
 Db 585 LISGILBFSKOPMLDHAYASKIGNKIDEWEKK-YGRNPFENGYDARHKAFLDFDSFLSSF 643  
 Qy 369 VISTLQYSKQMFHEVANKLNKIVEWENHGGNKFENYDARYLANLQDNMFLNL 428  
 Db 644 NKQYETERAVLFTQQRMDYIGELAGITGDKLSSGKAYVDYFQEGKLEKKPDDESKV 703  
 Qy 429 NKLQAEVSIATLQQMDNNTGDLAGISRGKSKVYDAFEPSKHI-KADKL-V 484  
 Db 704 VEDPTKGEDISNS-QPSTL-LKFVTPPLTPTESRVTQGKEYITKLVKGDKWV 761  
 Qy 485 QLDANGTIDDSNSGRAKTQHLFRPLLTPTEHERVQTYEITKLNNRVDWSWKI 544  
 Db 762 NGVKDKGAVYYDTNLIOHAHIS-SSVARGEEYREVLYSHLGNGNDKVFLAAGSAPIHAG 820  
 Qy 545 TOGAA-SSTDQTNWVORIGIELDNAGNVTKTKIAKJGEGDDNVFVSGBTEDGG 603  
 Db 821 EGHDVYYDQKTDGGLVIDGKTKATEGRYSVTRELSGATKLREVTKNQKAVGKREETL 880  
 Qy 604 EGYDRVHSRGNYGALTIDATKETEQCSYTVNR-FVETGKALHEYSTHTALVGNEEKI 662  
 Db 881 ENRDYELTQSGBMSNLKAHDLNLSVEET-GSNORDEFKSKFRDIFHGADGDDLNNGD 939  
 Qy 663 EXRHSN-NQH-HAGYTKDTLKAVEETIGTSHNDIEFKSKENDAFNGDGVDTIDGNDGN 720

RESULT 14  
 ID .PCT-US93-10500-2 STANDARD: PRT: 1244 AA.  
 XX  
 AC xxxxxx  
 XX  
 DT  
 XX  
 DE  
 XX  
 Sequence 2, Application PC/TUS9310500  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Chang, Yung-Tu  
 CC TITLE INVENTION: Recombinant Vaccine For Procine  
 CC NUMBER OF INVENTION: Pleuropneumoniae  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Alan S. Korman  
 CC STREET: 1600 Empire Tower  
 CC CITY: Buffalo  
 CC STATE: New York  
 CC COUNTRY: U.S.A.  
 CC ZIP: 14202  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/Ms-DOS  
 CC SOFTWARE: PatentIn Release #1.0, version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US93/10500  
 CC FILING DATE:  
 CC CLASSIFICATION:  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/972,229  
 CC FILING DATE: 05-NOV-1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Korman, Alan S.  
 CC REGISTRATION NUMBER: 33,932

QY 940 DILYGDKGNDIELRGDNGNDOLYGGEDKLLGGNNN YL - SGGDGND 985  
 QY 721 DRLEFGKGDDILDGGNGDFIDGKGNDLHGKGDDIFVRKGDGND 768

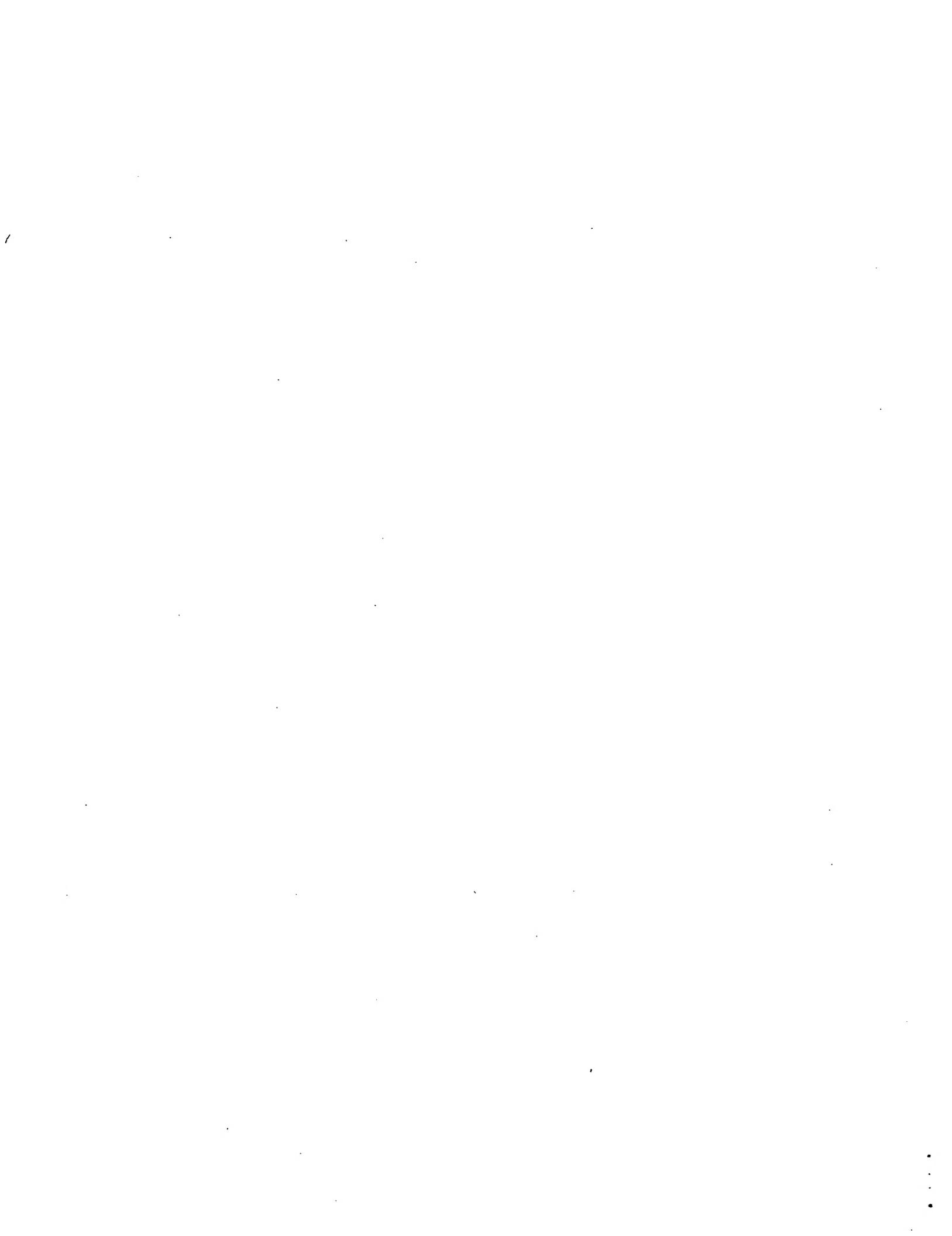
RESULT 15 ID US-08-387-156-10 STANDARD; PRT; 544 AA.  
 CC Patent No. 5/23129 Sequence 10, Application US/08387156  
 CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC ADDRESS: REDMOND, MARK J.  
 CC APPLICANT: HUGHES, HOW P.A.  
 CC TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS  
 CC NUMBER OF SEQUENCES: 28  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: REED & ROBINS  
 CC STREET: 635 BRYANT STREET  
 CC CITY: PALO ALTO  
 CC STATE: CALIFORNIA  
 CC COUNTRY: UNITED STATES OF AMERICA  
 CC ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0., Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/387,156  
 FILING DATE: 10-FEB-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/960,932  
 FILING DATE: 14-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/779,171  
 FILING DATE: 16-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ROBINS, ROBERTA L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/DOCKET NUMBER: 9901-0016-21  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 617-8999  
 TELEFAX: (415) 327-3231  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 544 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE: 544 AA; 57542 MW; 1502532 CN;

Query Match 36.0%; Score 2239; DB 1; Length 544;  
 Best Local Similarity 100%; Pred. No. 1.35e-153; Gaps 0;  
 Matches 351; Conservative 0; Mismatches 0; Indels 0;

Db 1 MATVIDLSPFKTGAKKIIYLIPQNYQDIEQNGNLQDLYKAAPELGIVQREERNNIATA 60  
 Qy 1 MATVIDLSPFKTGAKKIIYLIPQNYQDIEQNGNLQDLYKAAPELGIVQREERNNIATA 60  
 Db 61 QTSLGTTQTAIGLTGERGIVLsapQDkLQkTQAGQALGSAESTVNANKAKTVLSGIQS 120  
 Qy 61 QTSLGTTQTAIGLTGERGIVLsapQDkLQkTQAGQALGSAESTVNANKAKTVLSGIQS 120  
 Db 121 LGSVLAGMDLDEALQNSQHALAKAGBLTNSLIENANSVKTLDGEQISQFGSKL 180

QY 121 LGSVLAGMDLDEALQNSQHALAKAGBLTNSLIENANSVKTLDGEQISQFGSKL 180  
 Db 181 QNIKGJLGLGDKLNKNGLDKAGLGLDVISGLSSATAALYLDKNASTAKVGAGFELA 240  
 Qy 181 QNIKGJLGLGDKLNKNGLDKAGLGLDVISGLSSATAALYLDKNASTAKVGAGFELA 240  
 Db 241 NOVVGNITKAVSYIILQRYAAGLSSTPYAA LISTVSLAISPLAFAGTADKENHAKSL 300  
 Qy 241 NOVVGNITKAVSYIILQRYAAGLSSTPYAA LISTVSLAISPLAFAGTADKENHAKSL 300  
 Db 301 ESYAERFKKLQYGDGNLAEYORGTTIDASVTAINTLAAIAGGSAAAA 351  
 Qy 301 ESYAERFKKLQYGDGNLAEYORGTTIDASVTAINTLAAIAGGSAAAA 351

Search completed: Wed Dec 9 19:31:17 1998  
 Job time : 55 secs.





CC	LENGTH: 936 amino acids	RESULT 2	STANDARD;
CC	TYPE: amino acid	ID US-07-779-171-10	PRT;
CC	TOPOLOGY: linear	XX	936 AA.
SEQUENCE	936 AA; 100529 MW; 4311495 CN;	AC	
Query Match	100.0%; Score 6217; DB 8; Length 936;		
Best Local Similarity 100.0%; Pred. No. 0.00e+00;			
Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db 1 MATVIDLSFPTKAKKILYIIPONQYDTEBOGNGLQDLVKAEEELGIEYOREVERNNIATA 60	DE Sequence 10, Application US/07779171		
Qy 1 MATVIDLSFPTKAKKILYIIPONQYDTEBOGNGLQDLVKAEEELGIEYOREVERNNIATA 60	XX Sequence 10, Application US/07779171		
Db 61 QTSLGTTQTAIGLTERRGIVLSAPQIDKLQLQTKRAGQALGSAESYQNANKAKTVLGSQS 120	CC GENERAL INFORMATION:		
Qy 61 QTSLGTTQTAIGLTERRGIVLSAPQIDKLQLQTKRAGQALGSAESYQNANKAKTVLGSQS 120	CC APPLICANT: Potter, Andrew A.		
Db 121 ILSVSLAGMDLDEALQNNSNQHALAKAGLELTNSLIENIANSVKTLDERGEQISQFGSKL 180	CC APPLICANT: Redmond, Mark J.		
Qy 121 ILSVSLAGMDLDEALQNNSNQHALAKAGLELTNSLIENIANSVKTLDERGEQISQFGSKL 180	CC APPLICANT: Hughes, Huw P.A.		
Db 181 ONIKGLGTGSDKLKNIGGLDKAGLGLDVISGLSGATAAIVLADKNASPAKKYGAGFELA 240	CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING		
Qy 181 ONIKGLGTGSDKLKNIGGLDKAGLGLDVISGLSGATAAIVLADKNASPAKKYGAGFELA 240	CC NUMBER OF SEQUENCES: 14		
Db 241 NOVGNITKAVSYTLLAQRYANGLSSGTPYAALASTVSLAISPLAFLAGTADRENHAKSL 300	CC CORRESPONDENCE ADDRESS:		
Qy 241 NOVGNITKAVSYTLLAQRYANGLSSGTPYAALASTVSLAISPLAFLAGTADRENHAKSL 300	CC ADDRESS: Morrison & Foerster		
Db 301 ESYABRFKKGLYDGDNLLAFLYQRGTGTIDSATVNTALAAAGGVSAAAAGSYTASPIA 360	CC STREET: 545 Middlefield Road, Suite 200		
Qy 301 ESYABRFKKGLYDGDNLLAFLYQRGTGTIDSATVNTALAAAGGVSAAAAGSYTASPIA 360	CC CITY: Menlo Park		
Db 361 LLVSGTGTGVSTILOYSKQAMEHYANKTHNKIVEWEMKNHGKNYFENGYDARYLANLQD 420	CC STATE: California		
Qy 361 LLVSGTGTGVSTILOYSKQAMEHYANKTHNKIVEWEMKNHGKNYFENGYDARYLANLQD 420	CC COUNTRY: USA		
Db 421 NMKEFLNLNLKELQASRVIAITQQDNNNGDLAGISRLGDKVLGSKAYVDAFFEGKHKA 480	CC ZIP: 94025		
Qy 421 NMKEFLNLNLKELQASRVIAITQQDNNNGDLAGISRLGDKVLGSKAYVDAFFEGKHKA 480	CC COMPUTER: IBM PC Compatible		
Db 481 DKLVQLDSANGIIDVSNSGKAKTQHILFRPLPTEHRRVOTGKEYITKLNINRD 540	CC OPERATING SYSTEM: PC-DOS/MS-DOS		
Qy 481 DKLVQLDSANGIIDVSNSGKAKTQHILFRPLPTEHRRVOTGKEYITKLNINRD 540	CC SOFTWARE: Patent Release #1.0, Version #1.25		
Db 541 SWKITDGAASSTFDLTVNVRIGTNTKETLDNAGNTKETKTIKAKLGEGDDNVFGSGTTEI 600	CC CURRENT APPLICATION DATA:		
Qy 541 SWKITDGAASSTFDLTVNVRIGTNTKETLDNAGNTKETKTIKAKLGEGDDNVFGSGTTEI 600	CC APPLICATION NUMBER: US/07779171		
Db 601 DGEGYDPRHYSRGNYGALTIDAKETEQSYTNRVEFTGALKHEVSTHTLVGNREE 660	CC FILING DATE: 1991/10/16		
Qy 601 DGEGYDPRHYSRGNYGALTIDAKETEQSYTNRVEFTGALKHEVSTHTLVGNREE 660	CC CLASSIFICATION: 424		
Db 661 KIEYRHSNNOHHAGYTYKDTLKAVEBIIIGTSNDLFKGSKFNDAFNGDGVDTDGNDGN 720	CC ATTORNEY/AGENT INFORMATION:		
Qy 661 KIEYRHSNNOHHAGYTYKDTLKAVEBIIIGTSNDLFKGSKFNDAFNGDGVDTDGNDGN 720	CC NAME: Robins, Roberta L.		
Db 721 DRLFGGKGDIDLGCGNGNDLFTFGSKFNDAFNGDGVDTDGNDGN 780	CC REGISTRATION NUMBER: 33,208		
Qy 721 DRLFGGKGDIDLGCGNGNDLFTFGSKFNDAFNGDGVDTDGNDGN 780	CC TELECOMMUNICATION INFORMATION:		
Db 781 FDSNLKOLTFEKKHNLVITNSKEKVTIONWREADAKEPVNYKATKDEKEELIQ 840	CC TELEPHONE: 415-327-7250		
Qy 781 FDSNLKDLTFEKYKHNLTNSKEKVTIONWREADAKEPVNYKATKDEKEELIQ 840	CC TELEX: 415-327-2951		
Db 841 NGERITSKVQVDLIAKGNKQTQDSLSSQFARGSQHWSYGLRPG 916	CC INFORMATION FOR SEQ ID NO: 10:		
Qy 841 NGERITSKVQVDLIAKGNKQTQDSLSSQFARGSQHWSYGLRPG 916	CC SEQUENCE CHARACTERISTICS:		
Db 901 DSRYNLVAPTSMLDOSLSSQFARGSQHWSYGLRPG 936	CC LENGTH: 936 amino acids		
Qy 901 DSRYNLVAPTSMLDOSLSSQFARGSQHWSYGLRPG 936	CC TYPE: AMINO ACID		
Db 241 NOVGNITKAVSSYLLAQRAAGLSSTSOPVAALIYSTVSLAISPLAFAGTADKFNHAKSL 300	CC TOPOLOGY: linear		

QY 241 NOVGNITKAVSSYIILQRVAAGLSSTGPVALIASTVSLAISPLAFAGIADKFENHAKSL 300  
 DD 301 ESYAERFKLKGDDNLLAEYORGTTGTDASUTNINTALAAIAGGYSAAAGSVIASPIA 360  
 QY 301 ESYAERFKLKGDDNLLAEYORGTTGTDASUTNINTALAAIAGGYSAAAGSVIASPIA 360  
 DD 361 LIVSGTGVISTLQYSKOAMPEHVANKIHNNIVEWKNHKNYFENGYDARYLNLQD 420  
 QY 361 LIVSGTGVISTLQYSKOAMPEHVANKIHNNIVEWKNHKNYFENGYDARYLNLQD 420  
 DD 421 NMKFLLNKEQARVIAITOOQDNNIGDLAGISRLGEKYLGSKAYVDAFEFGHKIA 480  
 DD 421 NMKFLLNKEQARVIAITOOQDNNIGDLAGISRLGEKYLGSKAYVDAFEFGHKIA 480  
 QY 421 NMKFLLNKEQARVIAITOOQDNNIGDLAGISRLGEKYLGSKAYVDAFEFGHKIA 480  
 DD 481 DKLYQDSDANGLIDVSNSGSKAKTQHILFRPLTPTEHREVOTGRKEYTKLNVRD 540  
 QY 481 DKLYQDSDANGLIDVSNSGSKAKTQHILFRPLTPTEHREVOTGRKEYTKLNVRD 540  
 DB 541 SWKITDGAASSTEDLTNVQRGIELDAGNVTKTKEKTKIAKLGEODDNVEVGSGTTEI 600  
 QY 541 SWKITDGAASSTEDLTNVQRGIELDAGNVTKTKEKTKIAKLGEODDNVEVGSGTTEI 600  
 DB 601 DGGEGDVRHYSRGNYGALTIDATKETEQGNGTKEKTKIAKLGEODDNVEVGSGTTEI 660  
 QY 601 DGGEGDVRHYSRGNYGALTIDATKETEQGNGTKEKTKIAKLGEODDNVEVGSGTTEI 660  
 DB 661 KIEYRHSNNOHQHAGYTTKDLKAVEELIGTSNDIFGSKENDAFNGDGVTIDNDGN 720  
 QY 661 KIEYRHSNNOHQHAGYTTKDLKAVEELIGTSNDIFGSKENDAFNGDGVTIDNDGN 720  
 DD 721 DRLEGGKDDIDLGNGDDFIQGKGNDLFLHKGDDIITSGDNDKL 780  
 QY 721 DRLEGGKDDIDLGNGDDFIQGKGNDLFLHKGDDIITSGDNDKL 780  
 DB 781 FSDSNLKLDTFEVKHNLVITNSKKERTIONWREADFAKEPVNTKATDKDKEEELIQQ 840  
 QY 781 FSDSNLKLDTFEVKHNLVITNSKKERTIONWREADFAKEPVNTKATDKDKEEELIQQ 840  
 DB 841 NGRITSKQVDLJAKNGKTKODELSKVDYELKHSKNVNTSLDKLISSVSAFTSSN 900  
 QY 841 NGRITSKQVDLJAKNGKTKODELSKVDYELKHSKNVNTSLDKLISSVSAFTSSN 900  
 DB 901 DSRNVLVAPTMILDQSLSSLQFARGSHWSIGLRPG 936  
 QY 901 DSRNVLVAPTMILDQSLSSLQFARGSHWSIGLRPG 936

RESULT 3  
 ID US-09-124-491-8  
 DT XX  
 AC XXXXX  
 DE XX  
 Sequence 8, Application US/09124491

CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC TITLE OF INVENTION: GNAH - LEUKOTOXIN CHIMERA  
 CC NUMBER OF SEQUENCES: 34  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSE: REED & ROINS LLP  
 CC STREET: 285 HAMILTON AVENUE, SUITE 200  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 94301

CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: FLOPPY disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DO/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/09/124,491  
 CC FILING DATE:  
 CC CLASSIFICATION:  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/694,865  
 CC FILING DATE: 09-AUG-1996  
 CC APPLICATION NUMBER: US 08/387,156  
 CC FILING DATE: 10-FEB-1995  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/960,932  
 CC FILING DATE: 14-OCT-1992  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/779,171  
 CC FILING DATE: 16-OCT-1991  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: MCCRACKEN, THOMAS P.  
 CC REGISTRATION NUMBER: 38,548  
 CC REFERENCE/DOCKET NUMBER: 9001-0016-22  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415)327-3400  
 CC TELEFAX: (415)327-3231  
 CC INFORMATION FOR SEQ ID NO: 8:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 977 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 SQ SEQUENCE 977 AA: 104869 MW: 4761174 CN;

Query	Match	Score	Length
	100 %	6217	15;
Best Local Matches	100 %	Pred.	0
	0	Mismatches	0;
	0	Indels	0;
	0	Gaps	0;

DB 1 MATVIDLSPKTGAKKILYIPQNTQYDTEGNGLQDLVKAEEELGIVQEEREERNNTIA 60  
 QY 1 MATVIDLSPKTGAKKILYIPQNTQYDTEGNGLQDLVKAEEELGIVQEEREERNNTIA 60  
 DB 61 QTSLGTQTAGLTERGIVLSPAQIDKLQTKAGOALSASIVONAKRTVLGQS 120  
 QY 61 QTSLGTQTAGLTERGIVLSPAQIDKLQTKAGOALSASIVONAKRTVLGQS 120  
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 QY 121 ILGSVLAGMDIDEALONNSNQHALAKAGLETLTNSLTIENANSVKTIDFGQISOFGSKL 180  
 DB 181 QNKGLGTGDKLKNIGGLDAGLGLDVISLSSGATAVLADKNASTAKVGAFCFLA 240  
 QY 181 QNKGLGTGDKLKNIGGLDAGLGLDVISLSSGATAVLADKNASTAKVGAFCFLA 240  
 DB 241 NOVGNITKAVSSYIILQRVAAGLSSTGPVALIASTVSLAISPLAFAGIADKFENHAKSL 300  
 QY 241 NOVGNITKAVSSYIILQRVAAGLSSTGPVALIASTVSLAISPLAFAGIADKFENHAKSL 300  
 DB 301 ESYAERFKLKGDDNLLAEYORGTTGTDASVTAINTLAATAGGSVIASPIA 360  
 QY 301 ESYAERFKLKGDDNLLAEYORGTTGTDASVTAINTLAATAGGSVIASPIA 360  
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 QY 361 LLVSGTGVISTLQYSKQAMFEHVANKIHNNIVENKHHGKNYFENGYDARYLNLQD 420  
 DB 421 NMRFLLNKEIQAERYTATQQDWNIDLAGISRLGEKYLGSKAYVDAFEFGHKIA 480  
 QY 421 NMRFLLNKEIQAERYTATQQDWNIDLAGISRLGEKYLGSKAYVDAFEFGHKIA 480  
 DB 481 DKLYQDSDANGLIDVSNSGSKAKTQHILFRPLTPTEHREVOTGRKEYTKLNVRD 540  
 QY 481 DKLYQDSDANGLIDVSNSGSKAKTQHILFRPLTPTEHREVOTGRKEYTKLNVRD 540  
 DB 541 SWKIDGAASSSTFDLTVQRGIELDAGNVTKTKEKTKIAKLGEODDNVEVGSGTTEI 600

Qy 541 SWKITDGAASSTFDLTNVVORIGIEDDAGNVTKTKEKTLIAKLGEGLDDNVFVGSGTTEI 600  
 Db 601 DGEGYDRVHYSRGNYGALITDATETEQSYTVNREVENTKALHEVTSTHTALVGNEE 650  
 Qy 601 DGEGYDRVHYSRGNYGALITDATETEQSYTVNREVENTKALHEVTSTHTALVGNEE 650  
 Db 661 KIEYRHSNNQHAGYTAKDPLKAVEELIGTSNDLFGSKFNDAFNGDGTDTDGNDGN 720  
 Qy 661 KIEYRHSNNQHAGYTAKDPLKAVEELIGTSNDLFGSKFNDAFNGDGTDTDGNDGN 720  
 Db 721 DRLFGGKGDLDLGNGDDFTDGGKNDLHGKGDDIFYHRKGNDLITDSGNDKLS 780  
 Qy 721 DRLFGGKGDLDLGNGDDFTDGGKNDLHGKGDDIFYHRKGNDLITDSGNDKLS 780  
 Db 781 FDSNLKDLPFEVKHNLVITNSKEKVTIONWREADFAKEPVNKATKDEKEEEIGO 840  
 Qy 781 FDSNLKDLPFEVKHNLVITNSKEKVTIONWREADFAKEPVNKATKDEKEEEIGO 840  
 Db 841 NGERITSKQVDLIAKGNGKTDODELSKUVYDNEYLLKHSKNVNTSEDKLISVSASFSSN 900  
 Qy 841 NGERITSKQVDLIAKGNGKTDODELSKUVYDNEYLLKHSKNVNTSEDKLISVSASFSSN 900  
 Db 901 DSRNVLVAPTSMDLSSLOFARGSQHNSYGLRPG 936  
 Qy 901 DSRNVLVAPTSMDLSSLOFARGSQHNSYGLRPG 936

RESULT 4  
 ID US-08-694-865-8 STANDARD PRT: 977 AA.  
 XX AC xxxxx  
 XX DT NMKFLLNLKELOQERVINITQQWDNNGLAGSRLCKVLSGKAVYDAFECKHKA 420  
 DE Qy 361 LLVSGITGTVSTILQSKAMFEHVANKTHNKIVWEKNHKGNYFENGVDARYLANLGD 420  
 CC DB 421 NMKFLLNLKELOQERVINITQQWDNNGLAGSRLCKVLSGKAVYDAFECKHKA 480  
 CC DT Qy 361 LLVSGITGTVSTILQSKAMFEHVANKTHNKIVWEKNHKGNYFENGVDARYLANLGD 420  
 CC DB 421 NMKFLLNLKELOQERVINITQQWDNNGLAGSRLCKVLSGKAVYDAFECKHKA 480  
 CC DT Qy 361 LLVSGITGTVSTILQSKAMFEHVANKTHNKIVWEKNHKGNYFENGVDARYLANLGD 420  
 CC DB 421 NMKFLLNLKELOQERVINITQQWDNNGLAGSRLCKVLSGKAVYDAFECKHKA 480  
 Sequence 8, Application US/08694865  
 Sequence 8, Application US/08694865  
 GENERAL INFORMATION:  
 APPLICANT: POTTER, ANDREW A.  
 APPLICANT: MANN, JOHN G.  
 TITLE OF INVENTION: Gnr H-LEUKOTOXIN CHIMERAS  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: REED & ROBINS LLP  
 STREET: 285 HAMILTON AVENUE, SUITE 200  
 CITY: PALO ALTO  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-Dos/MS-Dos  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/694, 865  
 FILING DATE: 09-AUG-1996  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MCCRACKEN, THOMAS P.  
 REGISTRATION NUMBER: 38, 548  
 REFERENCE/DOCKET NUMBER: 9001-0016-22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415)327-3400  
 TELEFAX: (415)327-3231  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 977 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE 977 AA; 104869 MW; 4761174 CN;

Query Match Similarity 100.0%; Score 6217; DB 10; Length 977;  
 Best Local Similarity 100.0%; Pred. No. 0 00e+00; Mismatches 0; Indels 0; Gaps 0;  
 Matches 936; Conservative 0; Matrices 0;  
 Db 1 MATYIDLSPKTGAKKILYIPQNYQDYLWKAEEELGIEVOREERNNIATA 60  
 Qy 1 MATYIDLSPKTGAKKILYIPQNYQDYLWKAEEELGIEVOREERNNIATA 60  
 Db 61 QTSLGTTQAGLPERGTVISAPQDQLKQTKRGAQGSASESVQNANKAKTVLSGTQS 120  
 Qy 61 QTSLGTTQAGLTERGTVISAPQDQLKQTKRGAQGSASESVQNANKAKTVLSGTQS 120  
 Db 121 LGSVLAGMDDEALQNNSNQHALAKAGLELTNSLIENTANSYKTLDEFGQISQFGSKL 180  
 Qy 121 LGSVLAGMDDEALQNNSNQHALAKAGLELTNSLIENTANSVTLDEFGQISQFGSKL 180  
 Db 181 QNIKGLGTGDKLKNIGGLDKAGLGLDVSGLSGLSATAALVLADKNASTAKVYGAGFELA 240  
 Qy 181 QNIKGLGTGDKLKNIGGLDKAGLGLDVSGLSGLSATAALVLADKNASTAKVYGAGFELA 240  
 Db 241 NOVGNITKAVSSYLLAQVRAAGLSSTGVAALTASTYSLAISPLAFACIADKENHAKSL 300  
 Qy 241 NOVGNITKAVSSYLLAQVRAAGLSSTGVAALTASTYSLAISPLAFACIADKENHAKSL 300  
 Db 301 ESYAERFKLGYDGNLLAEYQRGTTIDASVTAINTALAAIAGVSAAAGSYTASPIA 360  
 Qy 301 ESYAERFKLGYDGNLLAEYQRGTTIDASVTAINTALAAIAGVSAAAGSYTASPIA 360  
 Db 361 LLVSGITGTVSTILQSKAMFEHVANKTHNKIVWEKNHKGNYFENGVDARYLANLGD 420  
 Qy 361 LLVSGITGTVSTILQSKAMFEHVANKTHNKIVWEKNHKGNYFENGVDARYLANLGD 420  
 Db 421 NMKFLLNLKELOQERVINITQQWDNNGLAGSRLCKVLSGKAVYDAFECKHKA 480  
 Qy 421 NMKFLLNLKELOQERVINITQQWDNNGLAGSRLCKVLSGKAVYDAFECKHKA 480  
 Db 481 DKVOLDSANGIIDVSNSKAKTOHILFLPTPLPTERRYOTGKYXITKLNINRD 540  
 Qy 481 DKVOLDSANGIIDVSNSKAKTOHILFLPTPLPTERRYOTGKYXITKLNINRD 540  
 Db 541 SWKITDGAASSTFDLTNVVORIGIELDNAGNVTKTETMIIAKLGEGDNVFVGSGTTEI 600  
 Qy 541 SWKITDGAASSTFDLTNVVORIGIELDNAGNVTKTETMIIAKLGEGDNVFVGSGTTEI 600  
 Db 601 DGGECDYDRHYSRGNYGALTIDATKETEGSYTINREVENTGKALHEVSTHTALVGNEE 660  
 Qy 601 DGGECDYDRHYSRGNYGALTIDATKETEGSYTINREVENTGKALHEVSTHTALVGNEE 660  
 Db 661 KIEYRHSNNOHAGYKTDLKAVEEITGTSNDLPGKSFNDAFNGGQVDTLGNDDN 720  
 Qy 661 KIEYRHSNNOHAGYKTDLKAVEEITGTSNDLPGKSFNDAFNGGQVDTLGNDDN 720  
 Db 721 DRLFGGKGDLDGNGDDFTDGGKNDLHGKGDDITVHRKGNDLITDSGNDKLS 780  
 Qy 721 DRLFGGKGDLDGNGDDFTDGGKNDLHGKGDDITVHRKGNDLITDSGNDKLS 780  
 Db 781 FSDSNLKDLPFEVKHNLVITNSKEKVTIONWREADFAKEPVNKATKDEKEEEIGO 840  
 Qy 781 FSDSNLKDLPFEVKHNLVITNSKEKVTIONWREADFAKEPVNKATKDEKEEEIGO 840  
 Db 841 NGERITSKQVDLIAKGNGKTDODELSKUVYDNEYLLKHSKNVNTSEDKLISVSASFSSN 900  
 Qy 841 NGERITSKQVDLIAKGNGKTDODELSKUVYDNEYLLKHSKNVNTSEDKLISVSASFSSN 900  
 Db 901 DSRNVLVAPTSMDLSSLOFARGSQHNSYGLRPG 936  
 Qy 901 DSRNVLVAPTSMDLSSLOFARGSQHNSYGLRPG 936

RESULT 5  
 ID US-08-878-748-8 STANDARD PRT: 977 AA.  
 XX AC xxxx

XX  
 DT  
 XX  
 DE  
 XX  
 CC Sequence 8, Application US/08878748  
 CC GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC APPLICANT: REDMOND, MARK J.  
 CC APPLICANT: HUGHES, HOW P.A.  
 CC TITLE OF INVENTION: GnrH-LEUKOTOXIN CHIMERAS  
 CC NUMBER OF SEQUENCES: 28  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: REED & ROBINS  
 CC STREET: 635 BRYANT STREET  
 CC CITY: PALO ALTO  
 CC STATE: CALIFORNIA  
 CC COUNTRY: UNITED STATES OF AMERICA  
 CC ZIP: 94101  
 COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentin Release #1.0, Version #1.2  
 CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/878,748  
 CC FILING DATE: 19-JUN-1997  
 CC CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/387,156  
 CC FILING DATE: 10-FEB-1995  
 CC APPLICATION NUMBER: US 07/960,932  
 CC FILING DATE: 14-OCT-1992  
 PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/779,171  
 CC FILING DATE: 16-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 CC NAME: ROBINS, ROBERTA L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE DOCKET NUMBER: 9001-0016 21  
 TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 617-8999  
 CC TELEFAX: (415) 327-3231  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 977 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 CC SEQUENCE 977 AA; 104869 MW; 4761174 CN;  
 SQ  
 Query Match 100.0%; Score 6217; DB 12; Len 61  
 Best Local Similarity 100.0%; Pred. No. 0.0e+00;  
 Matches 936; Conservative 0; Mismatches 0; II 61  
 1 MATVIDLSFPKTGAKKILYIPQNYQDTEQNGLQLDVLVKAELG  
 1 MATVIDLSFPKTGAKKILYIPQNYQDTEQNGLQLDVLVKAELG  
 Db 121 ILGSVLAGMDDEALQNNSNQHALAKAGLELTNSLIENIANSVTKTL  
 61 QTSLGTTQTAIGLTERGIVLSPAQIDLLQTKTGAQGLGSAESTVQI  
 61 QTSLGTTQTAIGLTERGIVLSPAQIDLLQTKTGAQGLGSAESTVQI  
 Qy 121 ILGSVLAGMDDEALQNNSNQHALAKAGLELTNSLIENIANSVTKTL  
 121 ONIKGIGLTGDKLNKGTDLQAGLGLDVLVSGLSSGPAULASVSLAISPL  
 Db 181 ONIKGIGLTGDKLNKGTDLQAGLGLDVLVSGLSSGPAULASVSLAISPL  
 181 ONIKGIGLTGDKLNKGTDLQAGLGLDVLVSGLSSGPAULASVSLAISPL  
 Qy 241 NOVGNITKAVSYTLAQRVIAQLGSSGPAULASVSLAISPL

QY	241	NOVGNGNITKAVSSYILLARORVAAGLSSTGPVALIATSYSLAISPLAFAGIADKINNAKSL	300
Db	301	ESYAERFKKLGYDGNLILAEYQRTGTIDASVTAINTALAAIAGSVAAAGSVIASPIA	360
QY	301	ESYAERFKKLGYDGNLILAEYQRTGTIDASVTAINTALAAIAGSVAAAGSVIASPIA	360
Db	361	LLVSGITGVISTLQYSQAMFHVANKIHNKIVEWKNHGNKYFENGVDARYLNLQD	420
QY	361	LLVSGITGVISTLQYSQAMFHVANKIHNKIVEWKNHGNKYFENGVDARYLNLQD	420
Db	421	NMKFLNLNLKELOAERYTAITQQWDNNNGDLAGISRLGEKVSKAYDAFEEGHKIA	480
QY	421	NMKFLNLNLKELOAERYTAITQQWDNNNGDLAGISRLGEKVSKAYDAFEEGHKIA	480
Db	481	DKLVQLDSANGILDVNSGSKARTQHILFRPLTPTEHRVQTGKYEITKLKNIRVD	540
QY	481	DKLVQLDSANGILDVNSGSKARTQHILFRPLTPTEHRVQTGKYEITKLKNIRVD	540
Db	541	SWRITDGAASSTEDLTNVQRIGIELDNAGNVTKTKEITKLAKJEGDDDNFVGSSTEI	600
QY	541	SWRITDGAASSTEDLTNVQRIGIELDNAGNVTKTKEITKLAKJEGDDDNFVGSSTEI	600
Db	601	DGEGDYDRHYSRGNYGALTIDATKETEGSYTYNRFVETGKALHEVTSTHTALVGNRE	660
QY	601	DGEGDYDRHYSRGNYGALTIDATKETEGSYTYNRFVETGKALHEVTSTHTALVGNRE	660
Db	661	KIEYRHSNQNHAGYYTDTLKAVEEITGTSHNDIFKGSKFNDAFNGGDGVTDGNDGN	720
QY	661	KIEYRHSNQNHAGYYTDTLKAVEEITGTSHNDIFKGSKFNDAFNGGDGVTDGNDGN	720
Db	721	DLRFGGKDDILDGGNGDDFDIGGGKNDLHGGKDDIFVHKGKDGNIDITSDGNDKLS	780
QY	721	DLRFGGKDDILDGGNGDDFDIGGGKNDLHGGKDDIFVHKGKDGNIDITSDGNDKLS	780
Db	781	FSDSNLKDLTFRVKHNUYTNSKKEKYTIONWFREADFAKEPVNPYKATDEKEIPIIGQ	840
QY	781	FSDSNLKDLTFRVKHNUYTNSKKEKYTIONWFREADFAKEPVNPYKATDEKEIPIIGQ	840
Db	841	NGERITSKQVDDLIAKGNGKITODELSKVDNDYELKHSKVNNTSLDKLJSSVSATFSSN	900
QY	841	NGERITSKQVDDLIAKGNGKITODELSKVDNDYELKHSKVNNTSLDKLJSSVSATFSSN	900
Db	901	DSRNVLYAPTSMLDQSLSLQFARGSHWSYGLRPG	936
QY	901	DSRNVLYAPTSMLDQSLSLQFARGSHWSYGLRPG	936
		RESULT 6 ID US-08-535-837-2 XX STANDARD: XX PRT; XX 926 AA. XX XXXXX	
		Sequence 2 , Application US/08535837 XX Sequence 2 , Application US/08535837 CC GENERAL INFORMATION: CC APPLICANT: POTTER, ANDREW A. CC ADDRESS: HARLAND, RICHARD J. CC TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE CC TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON - REGULATED PROTEINS CC NUMBER OF SEQUENCES: 6 CC CORRESPONDENCE ADDRESS: CC ADDRESSEE: ROBERTA L. ROBINS CC STREET: 285 HAMILTON AVENUE, SUITE 200 CC CITY: PALO ALTO CC STATE: CALIFORNIA CC COUNTRY: UNITED STATES OF AMERICA CC ZIP: 94301 CC COMPUTER READABLE FORM: CC MEDIUM TYPE: Floppy disk CC CONVENTIONAL: TTY, PC CC	

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/535, 837  
 FILING DATE: 27-SEP-1995  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ROBINS, ROBERTA L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/DOCKET NUMBER: 9001-0026.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 327-3400  
 TELEFAX: (415) 327-3331  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 926 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 LENGTH: 926 AA; MW: 4207190 CN;  
 SEQUENCE 926 AA: 99346 MW: 4207190 CN;

Query Match 98.5%; Score 6120; DB 9;  
 Best Local Similarity 100.0%; Pred. No. 0.0e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
 ID US-08-694-865-6 STANDARD; PRT; 926 AA.  
 XX  
 AC  
 XXXXX

Db 1 MATVIDLSPKTAGKKILYIPONQYDTEQNGLQDLVKAEEELGIEVDERERNNTATA 60  
 QY 1 MATVIDLSPKTAGKKILYIPONQYDTEQNGLQDLVKAEEELGIEVDERERNNTATA 60  
 Db 61 QTSLGQTIAIGLTTERGIVLSPAQIDKLQLQTKTAKAGQALGSAESIVQNANKAKTVLSGIQS 120  
 Qy 61 QTSLGQTIAIGLTTERGIVLSPAQIDKLQLQTKTAKAGQALGSAESIVQNANKAKTVLSGIQS 120  
 Db 121 ILSGYSLAGMDLDEALQNNSNHOHALAKAGLELTNLIENIANSVKTLDFFEQTSQFESKL 180  
 Qy 121 ILSGYSLAGMDLDEALQNNSNHOHALAKAGLELTNLIENIANSVKTLDFFEQTSQFESKL 180  
 Db 181 QNKGLGTLGDKLRNIGGLDAGLQGDTISLJSGATPAVLADKNASTAKVAGFELA 240  
 Qy 181 QNKGLGTLGDKLRNIGGLDAGLQGDTISLJSGATPAVLADKNASTAKVAGFELA 240  
 Db 241 NOVGNITPKAVSSYLAQRYVAAGLSSTGPVAALIATSYSLAISPLAFAGIAKFNHAKSL 300  
 Qy 241 NOVGNITPKAVSSYLAQRYVAAGLSSTGPVAALIATSYSLAISPLAFAGIAKFNHAKSL 300  
 Db 301 ESYAERFKLGYCDNLAEYQGTGTIDASVTAINTALAAGGSAAAASSVIASPIA 360  
 Qy 301 ESYAERFKLGYCDNLAEYQGTGTIDASVTAINTALAAGGSAAAASSVIASPIA 360  
 Db 361 LLYSGITGVISTLQYSKQMFHRVANKIHNVKIEWEKNHGRKYNFENGYDARYLANLQD 420  
 Qy 361 LLYSGITGVISTLQYSKQMFHRVANKIHNVKIEWEKNHGRKYNFENGYDARYLANLQD 420  
 Db 421 NMKFLLNLNKELOAERVIAITQQWDNNIGDLAGISRLGEKVLSKRAYDAFEKGHIKA 480  
 Qy 421 NMKFLLNLNKELOAERVIAITQQWDNNIGDLAGISRLGEKVLSKRAYDAFEKGHIKA 480  
 Db 541 SWKTDGAASSTDLTNVQRIQFIELDNAGNTKTKETKIIARLGEDDNVFGSGSTEI 600  
 Qy 541 SWKTDGAASSTDLTNVQRIQFIELDNAGNTKTKETKIIARLGEDDNVFGSGSTEI 600  
 Db 601 DGEGYDRHYHSRGNYGALTIDATKEEQGSYTVNRFVEGKALHEVTSHTHALYNRVD 600  
 Qy 601 DGEGYDRHYHSRGNYGALTIDATKEEQGSYTVNRFVEGKALHEVTSHTHALYNRVD 600  
 Db 661 KIEYRHSNQHQQHAGYTYDTLKAVEETIGTSNDIFGSKFENDAFNGGDYVTIDGNDGN 720  
 Qy 661 KIEYRHSNQHQQHAGYTYDTLKAVEETIGTSNDIFGSKFENDAFNGGDYVTIDGNDGN 720  
 Db 61 QTSLGQTQTAIGLTTERGIVLSPAQIDKLQLQTKTAKAGLGSAAEIVQNANKAKTVLSGIQS 120

Db 721 DRLFGGKGDILDGGNDDFTDGKGNDLZHGKGDDIFVHRKGDDIDITDSGNDKLS 780  
 Qy 721 DRFGGGDIDLGGNDDFTDGKGNDLZHGKGDDIFVHRKGDDIDITDSGNDKLS 780  
 Db 781 FSDSNLKDITFEVKHNLVITNSKKEVTONWREADAKEPVNYKATKDEKEIETIGQ 840  
 Qy 781 FSDSNLKDITFEVKHNLVITNSKKEVTONWREADAKEPVNYKATKDEKEIETIGQ 840  
 Db 841 NGERITSKQVDDLIARGNGKTODELSKVVNTELUKHSKNTNSLDKLSSVSAFTSSN 900  
 Qy 841 NGERITSKQVDDLIARGNGKTODELSKVVNTELUKHSKNTNSLDKLSSVSAFTSSN 900  
 Db 901 DSRNVLYAPTSMLDQSLSSLOFARGS 926  
 Qy 901 DSRNVLYAPTSMLDQSLSSLOFARGS 926

Sequence 6, Application US/08694865  
 Sequence 6, Application US/08694865  
 GENERAL INFORMATION:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/694, 865  
 FILING DATE: 09-AUG-1996  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MCCracken, Thomas P.  
 REGISTRATION NUMBER: 9001-0016.22  
 REFERENCE/DOCKET NUMBER: 9001-0016.22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415)327-3400  
 TELEFAX: (415)327-2331  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 926 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE 926 AA: 99346 MW: 4207190 CN;  
 Query Match 98.6%; Score 6128; DB 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 MATVIDLSPKTAGKKILYIPONQYDTEQNGLQDLVKAEEELGIEVDERERNNTATA 60  
 Qy 1 MATVIDLSPKTAGKKILYIPONQYDTEQNGLQDLVKAEEELGIEVDERERNNTATA 60  
 Db 61 QTSLGQTQTAIGLTTERGIVLSPAQIDKLQLQTKTAKAGLGSAAEIVQNANKAKTVLSGIQS 120

Qy 61 QTSGLGTQTAIGCLTERGIVLSSAPQIDKLLQKTKAGQALGSAEIVONANKVLSGIQS 120  
 Db 121 IIGSVLAGMDIDEALQNNSNQHALAKAGLETLNSLIENIANSVKTLDDEFQGQSGSKL 180  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 121 IIGSVLAGMDIDEALQNNSNQHALAKAGLETLNSLIENIANSVKTLDDEFQGQSGSKL 180  
 Db 181 QNKGKLGTLGDFLKNIGGLDKAGLGGLDVGIGLGSATAALYLADKNASTARKVAGFELA 240  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 181 QNKGKLGTLGDFLKNIGGLDKAGLGGLDVGIGLGSATAALYLADKNASTARKVAGFELA 240  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 241 NOVGNNTKAVSYILAQVRVAQLSSGTGPVALIAYSTVLASPLAFAGITADKFENHAKSL 300  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 241 NOVGNNTKAVSYILAQVRVAQLSSGTGPVALIAYSTVLASPLAFAGITADKFENHAKSL 300  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 301 ESYAERFKKLGVDGDNLAEYQRGTTGTDASATINTALAAGGYSAAAGSVIASPIA 360  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 301 ESYAERFKKLGVDGDNLAEYQRGTTGTDASATINTALAAGGYSAAAGSVIASPIA 360  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 361 LIVSGTGTGVISITLQSKOAMEHVANKIHNFIVEKENNIGKRYPENGTDARYLANLQD 420  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 361 LIVSGTGTGVISITLQSKOAMEHVANKIHNFIVEKENNIGKRYPENGTDARYLANLQD 420  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 421 NMKFLLNKEUNKEQAERTAITQOQDNNIGDAGISRLGEKVLGSKAYVDAEEGHKHA 480  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 421 NMKFLLNKEUNKEQAERTAITQOQDNNIGDAGISRLGEKVLGSKAYVDAEEGHKHA 480  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 481 DLKVOLDSANGIDVNSNGKAKTQHILLFRPTKERYXETKLNRVD 540  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 481 DLKVOLDSANGIDVNSNGKAKTQHILLFRPTKERYXETKLNRVD 540  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 541 SINKITDGASSFEDLTNVQRGIELDAGNVTKTKEPKTAKLKGESDDNVFGSGTEI 600  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 541 SWKITDGASSFEDLTNVQRGIELDAGNVTKTKEPKTAKLKGESDDNVFGSGTEI 600  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 601 DGGEGYDRHYSRGNYGALTIDATKETEQGSTVNRVEGTGKALHEVSTTHALYNRNE 660  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 601 DGGEGYDRHYSRGNYGALTIDATKETEQGSTVNRVEGTGKALHEVSTTHALYNRNE 660  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 661 KIEYRHNSNNOHQHAGYTTKDTLKAYVEETIGTSNDIFGSKENDAFNGGCVTIDGNQN 720  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 661 KIEYRHNSNNOHQHAGYTTKDTLKAYVEETIGTSNDIFGSKENDAFNGGCVTIDGNQN 720  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 721 DRFFGGKDDIDLGNGDDFTIGKGNDLFLHKGDDIDTIDSGNDNLS 780  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 721 DRFFGGKDDIDLGNGDDFTIGKGNDLFLHKGDDIDTIDSGNDNLS 780  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 781 FSDSNLKDLTFRVKHNLVITNSKKEVTRIONWREADFAKEVTPNKAQTKDKEIEETIQ 840  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 781 FSDSNLKDLTFRVKHNLVITNSKKEVTRIONWREADFAKEVTPNKAQTKDKEIEETIQ 840  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 841 NGERITSKQVDLIAKNGKTIQDELSKVVNDYELLKHSKNTNSLDKLSSVSATISSN 900  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 841 NGERITSKQVDLIAKNGKTIQDELSKVVNDYELLKHSKNTNSLDKLSSVSATISSN 900  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Db 901 DSRNVLVAPTMUDOSLSSLOFARG 926  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 901 DSRNVLVAPTMUDOSLSSLOFARG 926  
 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8  
 ID US-08-455-970-2  
 XX XXXXX  
 AC  
 DT  
 XX  
 DE  
 XX  
 Sequence 2, Application US/08455970  
 GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC APPLICANT: REDMUND, MARK J.  
 CC APPLICANT: HUGHES, HOW P.A.

Db	481	DKLVQDLSANGIIDVSNSGAKTQHILFRPLLTGTEHRVQTGKEYITKLINRYD	540
Qy	481	DKLVQDLSANGIIDVSNSGAKTQHILFRPLLTGTEHRVQTGKEYITKLINRYD	540
Db	541	SWKIDGAASSTFDLTVORIGIELDAGNVTKTKEKTIIAKLEGGDDNYFVGSGTTEI	600
Qy	541	SWKIDGAASSTFDLTVORIGIELDAGNVTKTKEKTIIAKLEGGDDNYFVGSGTTEI	600
Db	601	DGGEFYDRHV'SRGNYGALTIDATRETEEQSYTYRFETGKALEHTSTHALVGNREE	660
Qy	601	DGGEFYDRHV'SRGNYGALTIDATRETEEQSYTYRFETGKALEHTSTHALVGNREE	660
Db	661	KIEYRHSNNOHHAGYTTKDLKAVEBELLGTSNDLFKGSKFNDAFGNGDGVDTIDNGDN	720
Qy	661	KIEYRHSNNOHHAGYTTKDLKAVEBELLGTSNDLFKGSKFNDAFGNGDGVDTIDNGDN	720
Db	721	DRLFGKGDDILDGGNGDDFTDGKGNDLHGGKDDIFVHKGNDLITDSNDKLS	780
Qy	721	DRLFGKGDDILDGGNGDDFTDGKGNDLHGGKDDIFVHKGNDLITDSNDKLS	780
Db	781	FSDSNLKDLTFEKYRHLVINTSKKEKTVLQNWFREADFAKEPVNKATKDEKEIIGQ	840
Qy	781	FSDSNLKDLTFEKYRHLVINTSKKEKTVLQNWFREADFAKEPVNKATKDEKEIIGQ	840
Db	841	NGERTSKQVDLTLAKGNGKTQDLSKVYDNEYELIKHSKVNNTNSLDKLSSAFTSSN	900
Qy	841	NGERTSKQVDLTLAKGNGKTQDLSKVYDNEYELIKHSKVNNTNSLDKLSSAFTSSN	900
Db	901	DSRNVLVAPTSMLDSLSSLOFARS	926
Qy	901	DSRNVLVAPTSMLDSLSSLOFARS	926

RESULTS: 11S=0.8-878-718-6 STANDARD: BBT: 826 11

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X T X

Sequence 5: Application US 8887874 B

C TITLE OF INVENTION: GnRH-LEUKOTOXIN C

C CORRESPONDENCE ADDRESS:

C STREET: 635 BRYANT STREET

STATE: CALIFORNIA  
CITY: LOS ANGELES

COVINK: UNITED STATES OF AMERICA  
ZIP: 94301

COMPONENT READABLE FORM: MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC-MS-DOS

SOFTWARE: Patentin Release #1.0, Version 1.0

APPLICATION NUMBER: US/08/8/8, /48  
FILING DATE: 10-THUN-1007

CLASSIFICATION: 536  
APPROD APPROVAL: 5351

APPLICATION NUMBER: US 08/387,156

APPLICATION NUMBER: US 07/960,932

## PRIOR APPLICATION DATA:

C FILING DATE: 16-OCT-1991

CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: ROBINS, ROBERTA L.  
 CC REGISTRATION NUMBER: 33,208  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 671-8999  
 CC TELEFAX: (415) 327-3221  
 CC INFORMATION FOR SEQ ID NO: 6:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 926 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 SQ SEQUENCE:   
 926 AA; 99346 MW; 4207190 CN;  
  
 Query Match 926; Best Local Similarity 100.0%; Score 6128; Length 926;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Db 1 MATVIDLSEPKTGAKKKILYIPQNYQDTEQGNGLQDLVKAAELGIVQEERNNIATA  
 Qy 1 MATVIDLSEPKTGAKKKILYIPQNYQDTEQGNGLQDLVKAAELGIVQEERNNIATA  
  
 Db 61 QTSLGTTQAGLTERGYLSAPOIDKLQLKTAGQALGSAESIVQNANKAKTVLGSQ  
 Qy 61 QTSLGTTQAGLTERGYLSAQOIDKLQLKTAGQALGSAESIVQNANKAKTVLGSQ  
  
 Db 121 ILGSYLAGMDLDEALQNNNQHALAKAGLTLNSLIENANSYKTLDFEGEQISQFG5KL  
 Qy 121 ILGSYLAGMDLDEALQNNNQHALAKAGLTLNSLIENANSYKTLDFEGEQISQFG5KL  
  
 Db 121 QNKIGLGTGDKLKNIGGLDKAGLGLDVISGLSGATAALVLADKNASTAKKVAGFELA  
 Qy 121 QNKIGLGTGDKLKNIGGLDKAGLGLDVISGLSGATAALVLADKNASTAKKVAGFELA  
  
 Db 181 QNQVGNITAVSSTYLQARVAAGSISSTGPVAAILASTSLAISPLAFIGADFNHAKSL  
 Qy 181 QNQVGNITAVSSTYLQARVAAGSISSTGPVAAILASTSLAISPLAFIGADFNHAKSL  
  
 Db 241 NOVGNITAVSSTYLQARVAAGSISSTGPVAAILASTSLAISPLAFIGADFNHAKSL  
 Qy 241 NOVGNITAVSSTYLQARVAAGSISSTGPVAAILASTSLAISPLAFIGADFNHAKSL  
  
 Db 301 ESTAERFKLGYDGNLLAEYQRTGTIDA SVTAINTALAATAGGSVAAAGSVIASPIA  
 Qy 301 ESTAERFKLGYDGNLLAEYQRTGTIDA SVTAINTALAATAGGSVAAAGSVIASPIA  
  
 Db 361 LLVSGITGVSTILOYSKOMFEHVANKTHNKIVWEKHNNGK NYFENG DARYLANIQD  
 Qy 361 LLVSGITGVSTILOYSKOMFEHVANKTHNKIVWEKHNNGK NYFENG DARYLANIQD  
  
 Db 421 NMKEFLLNKELQERVIAITQQWDNNIGDLAGISRUGSKAYDFTEGKHAKA  
 Qy 421 NMKEFLLNKELQERVIAITQQWDNNIGDLAGISRUGSKAYDFTEGKHAKA  
  
 Db 481 DKLVQDSANGIIDYNSNGKAKTOHILFRPLUTPGTEHRERYTQGYEYTITKLININFVD  
 Qy 481 DKLVQDSANGIIDVNSNSKAKTOHILFRPLUTPGTEHRERYTQGYEYTITKLININFVD  
  
 Db 541 SWKTDGAASSTPDLNVYQRIQFIELDNAGNTKTKERKIIAKLGEGDDNNVFVGSGCTEI  
 Qy 541 SWKTDGAASSTPDLNVYQRIQFIELDNAGNTKTKERKIIAKLGEGDDNNVFVGSGCTEI  
  
 Db 601 DGGEQDYRHYSRQNYGALTIDATKETEGOVTGSHNDI FGSKENDAFNGDGVDTDGDN  
 Qy 601 DGGEQDYRHYSRQNYGALTIDATKETEGOVTGSHNDI FGSKENDAFNGDGVDTDGDN  
  
 Db 661 KIEYRHSSNQHQHAGYKTDLKAVEEIGTSHNDI FGSKENDAFNGDGVDTDGDN  
 Qy 661 KIEYRHSSNQHQHAGYYTDLKAVEEIGTSHNDI FGSKENDAFNGDGVDTDGDN  
  
 Db 721 DRFFGGKGDDILDGGNGDDFDIDGGKGNDLILHGKGDDLFYHRKGDNIDLTDSGDNDKL  
 Qy 721 DRFFGGKGDDILDGGNGDDFDIDGGKGNDLILHGKGDDLFYHRKGDNIDLTDSGDNDKL  
  
 Db 781 FSDSNKLDTFEKXKHNLVNTNSKERRKTTIQNWFREAFAKYEPNKKATKDEKTEIIGQ

Qy 781 FSDSNLKDLCVFKVHNVLITNSKEKVATIONWREADFAKEVPNYKATDKIEBFIGQ 840  
 DD 841 NGERITSKQDVDLIAKGNGKITQDELSKVVDYELHKSKNVTNSLDKLISSSAFTSSN 900  
 Qy 841 NGERITSKQDVDLIAKGNGKITQDELSKVVDYELHKSKNVTNSLDKLISSSAFTSSN 900  
 Db 901 DSRNVLYAPTSMDQSLSSLOFARG 926  
 Qy 901 DSRNVLYAPTSMDQSLSSLOFARG 926

RESULT 10 Application US/0779171  
 ID US-07-779-171-14 STANDARD PRT: 926 AA.  
 XX  
 DT  
 XX  
 DE Sequence 14, Application US/0779171  
 XX  
 CC Sequence 14, Application US/0779171  
 GENERAL INFORMATION:  
 CC APPLICANT: Potter, Andrew A.  
 CC APPLICANT: Redmond, Mark J.  
 CC APPLICANT: Hughes, Huw P.A.  
 CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING  
 CC NUMBER OF SEQUENCES: 14  
 CC ADDRESSEE: Morrison & Foerster  
 CC STREET: 545 Middlefield Road, Suite 200  
 CC STATE: Menlo Park  
 CC COUNTRY: California  
 CC ZIP: 94025  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/07/779-171  
 CC FILING DATE: 199106  
 CC CLASSIFICATION: 424  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Robins, Roberta L.  
 CC REGISTRATION NUMBER: 33, 208  
 CC FILING NUMBER: 29310-2001600  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415-327-7250  
 CC TELEX: 705141  
 CC INFORMATION FOR SEQ ID NO: 14:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 926 amino acids  
 CC TYPE: AMINO ACID  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 926 AA: 99346 MW: 4207190 CN;

Query Match 98.6%; Score 6128; DB 3; Length 926;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFPKIGAKKILYIIPONYQDTEQNGLQDLVAEELGIEVQREPERNNIATA 60  
 Qy 1 MATVIDLSFPKIGAKKILYIIPONYQDTEQNGLQDLVAEELGIEVQREPERNNIATA 60  
 Db 61 QTSUIGTQTAIGLTERGIVLSSAPQIDKLQTKAGQALGSNSIVQNANKATVLSIQS 120  
 Qy 61 QTSLGTQTAIGLTERGIVLSSAPQIDKLQTKAGQALGSNSIVQNANKATVLSIQS 120  
 Db 121 ILGSVLAGMDDEALQNSNQHALAKAGLELTNSLIENIANSVKTLDDEFGBISQFGSKL 180

Qy 121 ILGSVLAGMDDEALQNSNQHALAKAGLELTNSLIENIANSVKTLDDEFGBISQFGSKL 180  
 Db 181 QNIKGJLTDGLKNIGGLDKAGLGLDVSGLSGATAALVLDKNASTARKVGAGFELA 240  
 Qy 181 QNIKGJLTDGLKNIGGLDKAGLGLDVSGLSGATAALVLDKNASTARKVGAGFELA 240  
 Db 241 NOVVGNTKAVSSYTLAQRYAAGLSSSTGPYAAALIASTVSLAISPLAFAGIADKFENHAKSL 300  
 Qy 241 NOVVGNTKAVSSYTLAQRYAAGLSSSTGPYAAALIASTVSLAISPLAFAGIADKFENHAKSL 300  
 Db 301 ESYAERFKLGQYGDNLAAEYORGCTIDASVTANTALAAIAGYSAAAGSVIASPIA 360  
 Qy 301 ESYAERFKLGQYGDNLAAEYORGCTIDASVTANTALAAIAGYSAAAGSVIASPIA 360  
 Db 361 LLVSGITGVISTIQLQSKQAMFEYANKHNKIVEMKNNHGKNYFENGVDARYLANLQD 420  
 Qy 361 LLVSGITGVISTIQLQSKQAMFEYANKHNKIVEMKNNHGKNYFENGVDARYLANLQD 420  
 Db 421 NMKFLINLNKELOAERVATIQQQWDDNNIGDLAISRLGKAYDAFEEGHKIA 480  
 Qy 421 NMKFLINLNKELOAERVATIQQQWDDNNIGPLAGISRLGEVKLYFENGVDARYNE 480  
 Db 481 DKLVQLDSDANGIDYNSNSGRKAKTOHLLPPLTCPEHRRVQKYEYTKLNINRVD 540  
 Qy 481 DKLVQLDSDANGIDYNSNSGRKAKTOHLLPPLTCPEHRRVQKYEYTKLNINRVD 540  
 Db 541 SWKITDGASSTEDLTNVQRGIELDNAGNTVKTETKIKLAKLGEDDNFVGSTTEI 600  
 Qy 541 SWKITDGASSTEDLTNVQRGIELDNAGNTVKTETKIKLAKLGEDDNFVGSTTEI 600  
 Db 601 DGEGGYDRHYSRGNTYGAATDATKTEQGTYVNRFEVETKALHEVTSTHALYGNRE 660  
 Qy 601 DGEGGYDRHYSRGNTYGAATDATKTEQGTYVNRFEVETKALHEVTSTHALYGNRE 660  
 Db 661 KIEYRHSNNOHHAGGTYTKDTLKAVEEITGSHNDLFKGSKENDAFTGQYDTIDGNGN 720  
 Qy 661 KIEYRHSNNOHHAGGTYTKDTLKAVEEITGSHNDLFKGSKENDAFTGQYDTIDGNGN 720  
 Db 721 DRLEGGKQDDILDGGKNDLQGGKGDIDFVRKGDGNDITDSGDNLKS 780  
 Qy 721 DRLEGGKQDDILDGGKNDLQGGKGDIDFVRKGDGNDITDSGDNLKS 780  
 Db 781 FSDSNLKDLCFEVKHNLVTNSKERVETWREADFAKEPVNTKATDEKIEFIGQ 840  
 Qy 781 FSDSNLKDLCFEVKHNLVTNSKERVETWREADFAKEPVNTKATDEKIEFIGQ 840  
 Db 841 NGERITSKQVDDLIQNGKQTODELSKVVDNYELLKHSKNTNSLDLKLISVSAFTSSN 900  
 Qy 841 NGERITSKQVDDLIQNGKQTODELSKVVDNYELLKHSKNTNSLDLKLISVSAFTSSN 900  
 Db 901 DSRNVLYAPTSMDQSTSLSLQFARG 926  
 Qy 901 DSRNVLYAPTSMDQSTSLSLQFARG 926

RESULT 11  
 ID US-09-124-491-6 STANDARD PRT: 926 AA.  
 XX  
 AC XXXXXX

Sequence 6, Application US/09124491  
 Sequence 6, Application US/09124491  
 GENERAL INFORMATION:  
 APPLICANT: POTTER, ANDREW A.  
 APPLICANT: MANN, JOHN G.  
 TITLE OF INVENTION: GnRH-LEUKOTOXIN CHIMERAS  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: REED & ROBINS LLP

STREET: 285 HAMILTON AVENUE, SUITE 200  
 CC CITY: PALO ALTO  
 CC STATE: CA  
 CC COUNTRY: USA  
 CC ZIP: 94301  
 COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/09/124,491  
 CC FILING DATE:  
 CLASSIFICATION:  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: US 08/694,865  
 CC FILING DATE: 09-AUG-1996  
 CC APPLICATION NUMBER: US 08/387,156  
 CC FILING DATE: 10-FEB-1995  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/960,932  
 CC FILING DATE: 14-OCT-1992  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: US 07/779,171  
 CC FILING DATE: 16-OCT-1991  
 CC ATTORNEY/AGENT INFORMATION:  
 NAME: MCCRACKEN, THOMAS P.  
 REGISTRATION NUMBER: 38,548  
 REFERENCE/DOCKET NUMBER: 9001-0016-22  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415)327-3400  
 TELEFAX: (415)327-3231  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 926 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 CC SEQ ID NO: 99346 MW: 4207190 CN:  
 SEQ ID NO: 926 AA: 99346 MW: 4207190 CN:  
 Score 6128; DB 15; Length 926;  
 Best Local Similarity 100.0%;  
 Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Score 6128; DB 15; Length 926;  
 Best Local Similarity 100.0%;  
 Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 98.6%;  
 Best Local Similarity 100.0%;  
 Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MATVIDLSFKTAKKILLYPIQNYQDFTQGNGQDLVKAEEFLGIEQREERNNIATA 60  
 Qy 1 MATVIDLSFKTAKKILLYPIQNYQDFTQGNGQDLVKAEEFLGIEQREERNNIATA 60  
 Db 61 QTSLGTTAQLGLTERGIVLSPAQDILQLQTKTQAQLGSAESIVQNANKAKTVLSGQS 120  
 Qy 61 QTSLGTTAQLGLTERGIVLSPAQDILQLQTKTQAQLGSAESIVQNANKAKTVLSGQS 120  
 Db 121 ILSVSLAGMDIDEALONNSNOHALAKAGLETLNSLIENTANSVKTLDGEQISOFGSKL 180  
 Qy 121 ILSVSLAGMDIDEALONNSNOHALAKAGLETLNSLIENTANSVKTLDGEQISOFGSKL 180  
 Db 181 QNKIGLTGDLKKNIGGLDKAGLGLDVSGLSGATAALYADKNASPAKKVGAFFELA 240  
 Qy 181 QNKIGLTGDLKKNIGGLDKAGLGLDVSGLSGATAALYADKNASTKKVGAFFELA 240  
 Db 241 NQVGNNTKAVSYIQLQRYAAGLSSSTGPVAALISTVSLAISPLAFAGTADKNNHAKSL 300  
 Qy 241 NQVGNNTKAVSYIQLQRYAAGLSSSTGPVAALISTVSLAISPLAFAGTADKNNHAKSL 300  
 Db 301 ESYAERFKKUYGDNLNLAEYQRGTGTIDASVATNTALAAIAGEVSAAGSYIASPIA 360  
 Qy 301 ESYAERFKKUYGDNLNLAEYQRGTGTIDASVANTALAAIAGEVSAAGSYIASPIA 360  
 Db 361 LIVSGTGTGVISTLLOSKQAMFEHANKIINKIVWEKNNHGKMFENGYDARYLANLOD 420  
 Qy 361 LIVSGTGTGVISTLLOSKQAMFEHANKIINKIVWEKNNHGKMFENGYDARYLANLOD 420  
 Db 421 NMKFLLNKEQSERVIAITQOQWDNNIGDLAGISRLGEKVLSSKAYDAFEGKHika 480

Qy 421 NMKFLLNKEQSERVIAITQOQWDNNIGDLAGISRLGEKVLSSKAYDAFEGKHika 480  
 Db 481 DKLVQLDSSANGIIDVSNSSGAKTOHILFPTPLTPGTERERYOTGKYEYITKLNNIRVD 540  
 Qy 481 DKLVQLDSSANGIIDVSNSSGAKTOHILFPTPLTPGTERERYOTGKYEYITKLNNIRVD 540  
 Db 541 SWKTDGAASTSFEDLTNVQRTGFIELDNAGNYVKTKEFKIIAKLEGDDNFVGSQTTEI 600  
 Qy 541 SWKTDGAASTSFEDLTNVQRTGFIELDNAGNYVKTKEFKIIAKLEGDDNFVGSQTTEI 600  
 Db 601 DGGGYDRHYSRGNYGALTIDATKETEGSYYVNRVETGKALHEVTSTHTALVGNEE 660  
 Qy 601 DGGGYDRHYSRGNYGALTIDATKETEGSYYVNRVETGKALHEVTSTHTALVGNEE 660  
 Db 661 KIEYRHSSNQHAGYXTKTOLKAVEEITGTSNDIFGKSFKENDAFNGGDGVDTGNDNG 720  
 Qy 661 KIEYRHSSNQHAGYXTKTOLKAVEEITGTSNDIFGKSFKENDAFNGGDGVDTGNDNG 720  
 Db 721 DRLEGGKGDDILDGGNGDFFIDGGKGNDIITDSGNDKLS 780  
 Qy 721 DRLEGGKGDDILDGGNGDFFIDGGKGNDIITDSGNDKLS 780  
 Db 781 FSDSNLKDLTFERVKHNLVITNSKEKVKITIONWFREADAKEVPNYKATKDEKEEIQ 840  
 Qy 781 FSDSNLKDLTFERVKHNLVITNSKEKVKITIONWFREADAKEVPNYKATKDEKEEIQ 840  
 Db 841 NGERITSKQVDDLIAGNGKITQDELSKVVDNYELLKHSKNTNSLDKLISVSAFTSSN 900  
 Qy 841 NGERITSKQVDDLIAGNGKITQDELSKVVDNYELLKHSKNTNSLDKLISVSAFTSSN 900  
 Db 901 DSRNVLVAPTSMLDQSLSLQQFARG 926  
 Qy 901 DSRNVLVAPTSMLDQSLSLQQFARG 926

RESULT 12  
 ID US-08-455-970-10 STANDARD:  
 XX AC PRT:  
 XX xxxxx 943 AA.

Sequence 10, Application US/08455370  
 GENERAL INFORMATION:  
 CC APPLICANT: POTTER, ANDREW A.  
 CC APPLICANT: REDMOND, MARK J.  
 CC APPLICANT: HUGHES, HOW P.A.  
 CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN  
 CC NUMBER OF SEQUENCES: 15  
 CC CORRESPONDENCE ADDRESS:  
 STREET: 285 HAMILTON AVENUE, SUITE 200  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,970  
 FILING DATE: 31-MAY-1995  
 CLASIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/960, 932  
 FILING DATE: 14-OCT-1992  
 ATTORNEY/AGENT INFORMATION:  
 CC

NAME: ROBINS, ROBERTA L. 33,208  
 REGISTRATION NUMBER: 9001-0016.10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 327-3400  
 TELEFAX: (415) 327-3231  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 943 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE: 943 AA: 10129 MW: 4397993 CN:

Query Match 98 6%; Score 6128; DB 8; Length 943;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1 MATVDLSEPKTGAKKILYIPQNYQDTEQGNGLQLDVKAELGIEVQREBRNIAATA 60	Qy	1 MATVDLSPKTGAKKILYIPQNYQDTEQGNGLQLDVKAELGIEVQREBRNIAATA 60
Db	61 QTSLGQTQTAIGLTERGIVLSPAPIDKLQLQTKRGAOLGSAEVQNANKAKIVLSGIQS 120	Qy	61 QTSLGQTQTAIGLTERGIVLSPAPIDKLQLQTKRGAOLGSAEVQNANKAKIVLSGIQS 120
Db	121 IIGSVLAGMDIDEALQNSNOHALAKAGLETLNSLIENANTSYKTLDEFGEOISQFSKL 180	Qy	121 IIGSVLAGMDIDEALQNSNOHALAKAGLETLNSLIENANTSYKTLDEFGEOISQFSKL 180
Db	181 QNIKGLGTQDKLKKNIGLDKAGLJLDVTSGLSGATAALVLADKNASTAKVGAFFELA 240	Qy	181 QNIKGLGTQDKLKKNIGLDKAGLJLDVTSGLSGATAALVLADKNASTAKVGAFFELA 240
Db	241 NQVGNNTKAVSSYTLAQRAVAGLSSTGPVALIATSYLAIPLAFAGIAIDKFENHAKSL 300	Qy	241 NQVGNNTKAVSSYTLAQRAVAGLSSTGPVALIATSYLAIPLAFAGIAIDKFENHAKSL 300
Db	301 ESYAERFKLGYDGNLLAEYQRTGTTIDASVTAINTLAIAANGVSAAAGSVIASPIA 360	Qy	301 ESYAERFKLGYDGNLLAEYQRTGTTIDASVTAINTLAIAANGVSAAAGSVIASPIA 360
Db	361 LLVSGITGVSTILOYSKOAMEHVANKLNHKLVWEVKNNHGANFENGYDARYLANIQD 420	Qy	361 LLVSGITGVSTILOYSKOAMEHVANKLNHKLVWEVKNNHGANFENGYDARYLANIQD 420
Db	421 NMKEFLNLNKELOQERVTAITQWQDNNGDLAGISRLGEKTVLSKAVTDAFEKGHKKA 480	Qy	421 NMKEFLNLNKELOQERVTAITQWQDNNGDLAGISRLGEKTVLSKAVTDAFEKGHKKA 480
Db	481 DKLVOLDSANGIIDVSNSGKAKTOHILFRTPLTPGTEHRYRQTKKEYITKLINIRVD 540	Qy	481 DKLVOLDSANGIIDVSNSGKAKTOHILFRTPLTPGTEHRYRQTKKEYITKLINIRVD 540
Db	541 SWKTDGAASSTFDTNVQIGELDNRGNVTKTKEKILAKUGEDDDNFVFGSGTEI 600	Qy	541 SWKTDGAASSTFDTNVQIGELDNRGNVTKTKEKILAKUGEDDDNFVFGSGTEI 600
Db	601 DGGEQYDRHYSRGNYGALTIDATKETEGQSYTNRVETGKALHEVSTHTALVGNREE 660	Qy	601 DGGEQYDRHYSRGNYGALTIDATKETEGQSYTNRVETGKALHEVSTHTALVGNREE 660
Db	661 KIEYRHSNNOHHAGYYTKDYLKAVEEITGSHNDIEKGSKENDAENGDVDTIDGNQN 720	Qy	661 KIEYRHSNNOHHAGYYTKDYLKAVEEITGSHNDIEKGSKENDAENGDVDTIDGNQN 720
Db	721 DRLEGKGDDILDGNGDDEFDGKGNDLJHGKGDDLFVHRKGDNLDITSDGNDKLS 780	Qy	721 DRLEGKGDDILDGNGDDEFDGKGNDLJHGKGDDLFVHRKGDNLDITSDGNDKLS 780
Db	781 FDSNLKDLTFEKYKHNLYITNSKEKVYKTNRFVETGKALHEVSTHTALVGNRE 840	Qy	781 FDSNLKDLTFEKYKHNLYITNSKEKVYKTNRFVETGKALHEVSTHTALVGNRE 840
Db	781 FDSNLKDLTFEKYKHNLYITNSKEKVYKTNRFVETGKALHEVSTHTALVGNRE 840	Qy	781 FDSNLKDLTFEKYKHNLYITNSKEKVYKTNRFVETGKALHEVSTHTALVGNRE 840

RESULT<sup>13</sup>  
 ID US-07-779-171-12 STANDARD; PRT; 943 AA.  
 XX  
 AC XXXXXX

Sequence 12, Application US/07779171  
 GENERAL INFORMATION:  
 APPLICANT: Potter, Andrew A.  
 APPLICANT: Redmond, Mark J.  
 APPLICANT: Hughes, Huw P.A.  
 TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING  
 CHIMERICAS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Morrison & Foerster  
 STREET: 545 Middlefield Road, Suite 200  
 CITY: Menlo Park  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/779,171  
 FILING DATE: 19911016  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Robins, Roberta L.  
 REGISTRATION NUMBER: 293310-2001600  
 REFERENCE/DOCKET NUMBER: 293310-2001600  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-327-2750  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 943 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE 943 AA: 10129 MW: 4397993 CN;

Query Match 98 6%; Score 6128; DB 3; Length 943;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 926; Conservative 926; Mismatches 0; Indels 0; Gaps 0;  
 Db 61 QTSGTGTQTAIGLTERGIVLSPAPIDKLQTKAGAOQSAESIVNQNKAKTVLGSQ 120  
 Qy 61 QTSGTGTQTAIGLTERGIVLSPAPIDKLQTKAGAOQSAESIVNQNKAKTVLGSQ 120

Qy 1.21 IIGSVLAVGMDLDEALQNSNOHALAKAGLELTINSLIENIANSVKTLDDEFGEQISQFGSKL 180  
 Db 181 QNIKGLOTLGDKLNKNTGDLKNGLGIDLVGSGATAALVLAQDNASTARKVGAFELA 240  
 Qy 181 QNIKGLOTLGDKLNKNTGDLKNGLGIDLVGSGATAALVLAQDNASTARKVGAFELA 240  
 Db 241 NOYVGNTIKAVSSYLQRVAGLSSTGPVALIASTVSLSPLAFAGIADKENHAKSL 300  
 Qy 241 NOYVGNTIKAVSSYLQRVAGLSSTGPVALIASTVSLSPLAFAGIADKENHAKSL 300  
 Db 301 ESYAERFKKKLGDNILAEYORGTGTIDASVTAINTALAAIAGGSYAAAGSYIASPIA 360  
 Qy 301 ESYAERFKKKLGDNILAEYORGTGTIDASVTAINTALAAIAGGSYAAAGSYIASPIA 360  
 Db 421 NMKFLLNKLNEKLOAERYTATIQQQWNINIGDLAGISRLGEKVLSKRAYDAFEEGKHKA 480  
 Qy 421 NMKFLLNKLNEKLOAERYTATIQQQWNINIGDLAGISRLGEKVLSKRAYDAFEEGKHKA 480  
 Db 481 DKLVQLDSDANGIDVSNSGRAKTOHILLFRTPGTPEHRRVQTKYETIKLNINRVD 540  
 Qy 481 DKLVQLDSDANGIDVSNSGRAKTOHILLFRTPGTPEHRRVQTKYETIKLNINRVD 540  
 Db 541 SWKITGQAASSFEDLNIVQRGIELDAGTNVRFVQNNINGLAGTSRLGEKVLSGRAYVIAFEERKHRA 600  
 Qy 541 SWKITGQAASSFEDLNIVQRGIELDAGTNVRFVQNNINGLAGTSRLGEKVLSGRAYVIAFEERKHRA 600  
 Db 601 DGEGYDRVHYSRGNYGALTIDATKETEOGSXTYNRFVETGKALHEVTSTHTALVNREE 660  
 Qy 601 DGEGYDRVHYSRGNYGALTIDATKETEOGSXTYNRFVETGKALHEVTSTHTALVNREE 660  
 Db 661 KIEYRHSNNNOHHAGYTTKDTLKAYERLTGTSNDLFKGSKFNDAFNGDGYTDIDGNDEN 720  
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 Db 721 DRLFGGKDDILDGGNDDFLDGKNDLHLGGKDDIFHRKGONDITDSGNDKLS 780  
 Qy 721 DRLFGGKDDILDGGNDDFLDGKNDLHLGGKDDIFHRKGONDITDSGNDKLS 780  
 Db 781 FDSNKLKDTEPKVKHNLVTKRKERTVIONFREADFAKEPVNKATDEKEEIIQG 840  
 Qy 781 FDSNKLKDTEPKVKHNLVTKRKERTVIONFREADFAKEPVNKATDEKEEIIQG 840  
 Db 841 NCERITSKVQDPLIANGKNTQTKDLSKVYDNELLKHSKNTNSLDKLISSVSAFTSSN 900  
 Qy 841 NCERITSKVQDPLIANGKNTQTKDLSKVYDNELLKHSKNTNSLDKLISSVSAFTSSN 900  
 Db 901 DSRNVLVAPTSMDQSLSSOFARG 926  
 Qy 901 DSRNVLVAPTSMDQSLSSOFARG 926

RESULT <sup>14</sup>  
 ID US-07-77917-8 STANDARD PRT: 951 AA.  
 XX XXXXXXXX  
 AC  
 DT  
 XX  
 DE Sequence 8, Application US/0777917-8  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Potter, Andrew A.  
 CC APPLICANT: Redmond, Mark J.  
 CC APPLICANT: Hughes, Huw P.A.  
 CC TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING  
 CC TITLE OF INVENTION: PASTEURELLA HEMOLYTICA LEUKOTOXIN CHIMERA'S  
 CC NUMBER OF SEQUENCES: 14  
 CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Morrison & Foerster  
 CC STREET: 545 Middlefield Road, Suite 200  
 CC CITY: Menlo Park  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94025  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/07/779,171  
 CC FILING DATE: 1991/01/16  
 CC CLASSIFICATION: 424  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Robins, Roberta L.  
 CC REFERENCE/DOCKET NUMBER: 29310-2001600  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415-327-7250  
 CC TELEFAX: 415-327-2951  
 CC TELEX: 706141  
 CC INFORMATION FOR SEQ ID NO: 8:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 951 amino acids  
 CC TOPOLogy: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE: 951 AA; 10218 MW; 446354 CN;

Query Match 98.6%; Score 6128; DB 3; Length 951;  
 Best Local Similarity 100.0%; Pred. No. 0; 0.00e+00;  
 Matches 926; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

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 Qy 1 MATVIDLSPKTKGAKKIIYIPQNYQDYDEQGNSLQDLYVKAEEBLGIEVQREERNNTIA 60  
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 Qy 61 QTSLGQTIAIGLTERGIVTSLAPOSIDKLIQKTAGQALGSAESTYQNANKAKTVLSGIQS 120  
 Db 121 ILGSVLAGMDLDEALQNSNQHALAKAGLELTNSLIENIANSVKTLDDEQEIQSFGSKL 180  
 Qy 121 ILGSVLAGMDLDEALQNSNQHALAKAGLELTNSLIENIANSVKTLDDEQEIQSFGSKL 180  
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 Qy 121 ILGSVLAGMDLDEALQNSNQHALAKAGLELTNSLIENIANSVKTLDDEQEIQSFGSKL 180  
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 Qy 301 ESYAERFKLGYGDNLIALEYRGTTGTDASVTAINTLAAIINGVSAAGSVIASPIA 360  
 Db 361 LLVSGITGVISTILQYSKAMFEVANKHNKIVWEKNHGNRYFENGVDAYLANLQD 420  
 Qy 361 LLVSGITGVISTILQYSKAMFEVANKHNKIVWEKNHGNRYFENGVDAYLANLQD 420  
 Db 421 NMKEFLNKLQELQAEVIAITOCQWDNNNGDLAGISRGKAVYDAFFEGKHKA 480  
 Qy 421 NMKEFLNKLQELQAEVIAITOCQWDNNNGDLAGISRGKAVYDAFFEGKHKA 480  
 Db 481 DKLYQLDSSANGIDVSNCKAKTOHILLFRTPGTPEHRRVQTKYEVTKLNINRVD 540  
 Qy 481 DKLYQLDSSANGIDVSNCKAKTOHILLFRTPGTPEHRRVQTKYEVTKLNINRVD 540  
 Db 541 SWKTDGAASSTFDLTNVQRIEGLDNAGNTKTKTIIAKUGDDNFVFGSGTEI 600  
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Page 14

Search completed: Wed Dec 9 19:35:47 1998  
Job time : 252 secs.